

1198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TATTTATATT TTTTATCTC TGGCATACTT TGATACCTTT TAGACTTAA AGTCCTTAA	60
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TTTAAACCTT TCTGCTCTAG TTGCTCTTAA TCTCTCTCAT ACCATTTTAA GATTGTCCACA	180
TAGTGGTCTT GATAGGCTTT ACCACTGCTT TCCATGTATC TGGATAGTTT ATTTATCAAT	240
ATATCTGTGT GTGAGTTTAA TTTTCTTTTT AGATTITTAT ATCTCTCTTT GCTTAACCTT	300
ACATTTTGA ATCTCCATA AAAAATGGGG GTGGACTTTT TATCTATCTC TCCCTCTCTC	360
TCTTTATCTA TCTCTATATC TTTCATGTA ATTCCAATCT GGAGTACCTC TACTGTCTAT	420
CGTAAATTTA ATTTTGATAT CTGGCAATAC TGTGCTAGAT ATTGTATCTT TATATTCAAGT	480
ATTTTTTAAA GCTTGCCTAA TAATTGAAGT TAAATAGAAT GCTACTCTTT TATTCAATTC	540
TTTATTTTTT AATTTTAAAC AATGAATTTT CATATCTAGG CTGCTTTTAT ATTTATGATA	600
AAAGACTGCT CCTAAAAATG AAACAGATAT AAAATTTTCA AAACTCTAT AATTTTCTAT	660
ATCTATATCT TCGTAGTAAC CTAAGATACC ATGTCTCAAT TTGTAGCAC TAATCTTAGG	720
AGTTTTTCCA TCGAGTAAAT ATCTTTTGG AATAGATGAG CTTGTGGTA CTTAACTCGA	780
TTTCCCTCTT TTTTGGTAA TAAATATTC TTTTATTTT GTTGTCTGAT ATTTTCTCTA	840
CTGTGCTCTT GTAGGATGAG TATTTTCTAG ATTTTCYTGA ATAACTTTT ACPTGAAGTT	900
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ATATTGCTGT TATCTCTAT ATCTTAATTT TCATTCATGA TATCTTTTAA CTAATTTTAT	1020
CTTAAATTTT GTGCTGTAAT TGCCATTAAG AAACCTGACC CTTTATCTTA GTTTTCTGGC	1080
CTAACTTTTG AGGCTCAAGT CAJAAATTTG GACTTTTAAA TGAATTTCAA TATTCATTTA	1140
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ACGTATAATT TTTGCTTCAA GATTAAAGAT ATCTTTAACT AGTTTATCAT TTAGTATATC	1260
TTCAAGCTTT CCGTCTGCAA CAAGTTTACC TTTCTTAAAT GCAAATAGGT AATCAGCGTA	1320
TCTGCTGTGT AGATTATAT CTGCAAAAT CATGCAAAAT GTTGCTTTAT ATTTTGGTT	1380
TAGATCAGTC AAGAGGCTTA ATAGTCTCTAT TTGATATGAG ATATCCAAGT AAGTATGTTG	1440
CTCATCTAAA AGTAGGATAC TTGTATCTTG GCGTAGGGCT AGAGCTATCC ATACTCTTTG	1500
CTTTTACCCC CCAGAAAGTT CTCAACTAG GTTATTTGCT AGATCTTCAA CATTTGCGCTT	1560
AACCATTTGAT CTGTTTATTA TTTCAGGTC ATCTTTTCCA AGACTCTTAA AAGGCTTTCT	1620
GTAGGGGAAA CGACCAAGGC TTACAAGATC AGCTACTGTT ATTGATTCAG GGATTTATGG	1680
AGATTGAGGT AATATAGCTA TGTGTTTTCG TAAATCTTTT TCTTATAAG AATTAAATGA	1740

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GAGTGTGTGAT TTTCCACAAC CATTTGACCC AATTAATAACT GATATTTTTT CTTCAGGTAT	1860
TTTTATATTT ATATTTTCCA AGATTATTTT TTTCATCATAA CCGCAGGTAA GATTATTTGA	1920
CCACAGACCT TTCATTATAT ATTCCTCCTG TTCATTTTTA TTAGTAAGTA TATTAAGTAT	1980
GGTGAACCTA ACAAGCCAGT TACAACACCT ACTGGATATC TAGCTGGTAA AATATTTTGA	2040
GAGAAATATGT CTGATAACAA AACTAGTAAA ATTCCAACCA ATCCAGCTAA TATTTGGGCTT	2100
CTTTCTTGCG CAATATTTAA GGCTATGGGA CCAGCTAAAA AAGATATACA AGCTATTGGT	2160
CCTGTAAATTG AAGTAGAAAA AGCAGTTAAA GATACAGCGC AAAAAATTA AACAAGCCTT	2220
GAAAGCTCGG GATTTGCTCC AAGTCCGATT GCTATTCTCT CACCAAGTTC AATAATTTCT	2280
AGTCTTTTAT TAAAAAATAA AACTAATATA GTAGCAATAA TACTTACTAT TAGAACAAGA	2340
GGTATGTCAT CTAACCTTGT AAAAGATAAA GAGCACTGA GCCATCTCAT AACTTCTTGT	2400
AATTCATATC TTGCTACTTT CAACAATAAA AATGAGGTGC CTGCTCTTGT GACAGCTTGA	2460
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AATAATATTA AAGATGATGT TAGTCCACAA GTTATTGAAA TAAATCCAGT AGTTAAACTA	2580
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ATTATATCAG GACTTGCAAG AGGATTTCCT AACATAGTTT GAAAGATAAA TCTGCCAAAT	2700
CCAAAGACC AGCCAGCTAT AATCCTGCT AATAATTTTG GTAATCTAAT TTCCATAATC	2760
GAAAACTAG CTCCAGGAAC AGTTTCACTA TTTAAGACTT TAATCAAAGT TGAAAAAGAA	2820
TAACCTTCAT CTCCGATAAG TAAATGAAA AATGATAGAC TGATTATTAT TAATAAAAAAT	2880
AGTGAGGAAA ATAGTGTAT TCTATTTTTT CTTTTTGAA TACCTATAAT TAAATTTTGC	2940
ATTAGTTATT AACCCTCTTA TTTTTCATAG TTACATAAAT AAGTACTGGA CCCCAGATTA	3000
TTGCAGTAAT TATCCCTACT TCAATTTTCA CTGGTTTACC TAACATACGG CCGATTATAT	3060
CACATATAAG CAAGAGCTCT GCACCTATAA AAGATGAAGA AATGGTCAIT GTGCGTATAT	3120
CTTTGCTTAT AAATAAGCCA CAAAAGTGAG GAACTATAAG ACCTAGGAAG CCAATAGGTC	3180
CACCAATTCG AGTAATACTT GAACATAAAA GCACACTTGC AATTATTGCA AGTGATCTTA	3240
TCTATTATAC ATTAACTCCA AGACCAACAG CCATTTATC ACCCATAGCT AAAGCGTTTA	3300
AATCTGATGA AATTAATATA GCTATCAAGT GACCTAAAA TATAAAAGGT AGTAGTGTAG	3360
ATATAGAAGA TAATGTAGCT GCTCCAAGGC TACCTATTTG CCAAAATCTA AATTGTCTA	3420
AGAGTTATTT ATTCTGTAAG AATTAAAAAC TTACAAAATCT GCTTAAAGCC ATACTAACAC	3480

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AAGTTCCTGA TAAGGCAAGT TTTATAGGGG TAAGGCTTGC TTTTCGGTTA CAGCAATCGC	3540
GTATACAAAA ATTGCACCTTA CTAAAGCCACC AATGATTGCG	3580

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

CCAAATTGCT CCACAAATTAT TATGGAGTCG TCGTTTGSCA GATGGCCGTG ATATGTGTGC	60
TCAAGAATGG TTGACAGGCA AGATATTGAC CCCCTATGAT ATGAATCGTA AGCAAAATCGT	120
CAATATTTTA ACCCGTCTTC ATCGCTCAGC TCGTTTGATG ACACAATTGA GTCGTTTGGG	180
CTATGCCATG GAAACACCTG TAGATTACT ACAGTCTTGG CAGGAACGG CTCCAGATGC	240
TTTGGCTAAA AATCATTTTA TCAGTGAAGT GATGGCTGAT TTACGTGAGA CTATTCACGG	300
ATTTAGAGAG GACCATGCGA CCATTGTCCA TGGAGATGTA CGACATAGTA ATTGATTGA	360
GACAGATAGT GCGTTGATTT ATTTAGTAGA TTGGGATTGG GTTCGCTTGA CCGATCGCAT	420
GTTTGATGTG GCCCATATGC TCTGCCATTA TATTTAGAAA CATCAGTGGG AGGAATGGTT	480
GACCTACTAC GGTACAACT ACAATCAAAC GGTATTAAGT AAATGTATTT GGTATGGTCA	540
ATTGTCTTAT TTGAATCAGA TTTCCAAGTA TTATATGAAC CAAAGATTAG AAAATGTCAA	600
TGCGGAGATT CATGGTTTGC GTCAATTTCC AGACAAGTAT GGAAAGAGAA GATGAGAGTT	660
AGAAATCGTA AAGGGGCAAC AGAATTACTA GAGGCAAAAT CCCAGTATGT GGTCTCTAAT	720
CCCTTGGAA G CCAAGGCAAA ATGGCGGGAC TTGTTTTGCA ATGATATCC CATTCATGTG	780
GAAGTTGGAA GTGGAAAGGG TGCCTTTGTG TCAGGTATGG CCAAGCAAAA CCCTGACATC	840
AACTATATCG GAATTGATAT TCAAAAGTCT GTTTGAGCT ACGCTTTGGA CAAGGTGCTT	900
GAAGTTGGAG TGCCTAACAT CAAGCTCTTG TGGTAGATG GTTCTGACTT AACTGACTAC	960
TTTGAGACG GTGAGATTGA TCGCTTGAT CTGAACCTTT CAGATCCATG GCCGAAAAAA	1020
CGCCATGAAA AGCGTCGTTT GACCTACAAG ACCCTCTTGG ATACCTTCAA ACGTATCTTG	1080
CTTGAAAATG GAGAAATCCA TTTCAAGACG GATTAACGCG GCTTGTTTGA GTACAGTTTA	1140
GTGAGCTTTT CTCATATGG CATGAAACTC AATGGTGTCT GGTAGATTTC GCATGCCAGT	1200
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ATCTACCGAG TTGAGGCAGA ATTTTAAGAG ATAACCTAAA ATTAGGCTGT ACAAGTGTCT	1320

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TAGTCAGAGA AGTTGTAGAA CCTGTCATAG AAGCTCCTTT TGAATCGTG GATATCGAGT	1500
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CTTGAACGAC ACGCGAGCT TGACAGAAAT TATCAGTCCT GTCCATAGACA CCATCAAGCC	1620
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GAAACCAAG GATGCCCTCG CTGGAACGGT TGGAAATATC ATCCATGTGG GCTCTACCA	1740
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CGCAATTTGA AGCCATGGAA GACGCTGCTT CAGTAGAGTT GGAAGTAGAA AACGATACTG	3060

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AGGAAGGACA	AGTCTTTAT	GATCCTACGG	GCAAGGCCAA	TGGCCGCGGC	GCTTATATCA	3240
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GCCAAAGTTG	TCTTTCTAGC	TCATGATGCT	GGACCCAATC	TGACCAAGAA	GATTCAAGAT	3540
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TCAGAAAAAC	GACGCCGCTA	ATGTTGGAAA	ACAAGGTCAA	AGCAACCGCG	ACAATCGTGG	4260
CTTTAATGAC	CAMGTAAAGA	AGCAGCAAGG	TCAGCAAAAA	CGTAGAAATG	AGCGCCGTCA	4320
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CGTCCCTGAG	AAAAAAGAAC	CTGCAGTGGA	TACACGTCGT	AAAAAACAA	CTGCACCAAG	4620
CAAAAATCGT	GACGATTATG	ATCATGAAGA	AGATGCTCCT	AGAAAAACAA	AAAGAAATCG	4680
AAGTAGTCAA	AATCAAGTGA	GAAATCAAAA	GAAATAGTAA	TGGAATAACA	ACAAAAAGAA	4740
CAAAAAAGGC	AATAAACAAG	ACAACCGTAA	TCAGACTCCA	AAACCTGTTA	CGGAGCGTAA	4800
ATTTCATGAA	TTGCCAACAG	AATTTGAATA	TACAGATGGT	ATGACCGTTG	CGGAAATCOC	4860

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 TATCGAAGCC AAACAAAAGG TTGAAGTGGG TAAAGCTGAC ATCGAACGTT TCTTTGTCGA 5040
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 ACACGTTGAC CACGGTAAAA CAACCCCTTT GGATACTCTT CGTAACTCAC GTGTTGCGAC 5160
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 TGATGGTGAA CTGCAAGCT TCAAACTA TAAGAGCGAC GTGAAGAAG TGACAAACGG 6480
 TCGTGAAGGT GGATTGATGA TCGACGGCTA CAATGATATT AAGATGATG ATGTGATTGA 6540
 GCGGTATGTC ATGGAAGAAA TCAAGAGATA AGATTTTGTG CTCCTTCTTT AGGTGATGAG 6600

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TTCAAATGGA	ACTTCGTTTC	AATTTAAACT	GAAAATCAAG	AAGTTTAAAA	TAGCTAGGTC	6780
TGCTGGCCTA	GCTTTTGCTT	CAAAAGTAGAG	AAAGGAATAT	CATGGCAAAAT	CATTTCCGTA	6840
CAGATCGTGT	GGGCATGGAA	ATCAAGCGTG	AAGTCAATGA	GATTTTGCAA	AAGAAGTCC	6900
GTGATCCAGC	TGTCCAAGGT	GTGACCATCA	TAGATGTTCA	GATGCTGGGT	GACTGTGCTG	6960
TTGCCAAGGT	TTATTAACCC	ATTTTGAGTA	ACCTTGCTTC	GGATAACCAA	AAAGCCCAAA	7020
TCGGGCTTGA	AAAAGCAACT	GGTACCATCA	AACGTGAAC	TGGTCGCAAT	TTGAAATTGT	7080
ACAAAATCCC	AGATTTTGAC	TTGCTCAAAG	ACGAGTCCAT	CGAGTATGGA	AACAAGATTG	7140
ACGAGATGCT	ACGCAATCTG	GATAAGAACT	AAAGAAGAGG	GGTTCGCCCT	CTTTTTTGCT	7200
GGAGGAAAT	AGCTTGAAT	TGAAATGGAA	AAATATTCCT	TTATTAATAGA	TTGAAACTAG	7260
AAATAGTACG	CTCTACTCT	AAAATATTGT	TAGAAATCGA	TTTACTGTTC	CTGATCGAAT	7320
TGTCTCTGTC	TTGTTTCATT	TAAATATAAA	AAAGGGATTC	TGTATTTTTC	AATGTTATCT	7380
AATTAGAAAA	TGCTTTTTTC	GTAGGAATA	TAATATGATA	AGGTGCAAAA	AAGAAATAAG	7440
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ACCTGTGTGT	AAGGTTGATC	GTTGAAATTT	TTTAGTGGAT	AAGTTTTCCT	AAGAATTGGA	7560
TCCAAAAGAT	ATTCTACCT	TATTGGAACA	AGGTCCAACG	ACTCTTCTAT	CTCAAGAAAT	7620
ATTAGATCGT	GTAGCTAATG	CTTGATTTCC	GGACAATGTA	TTATTAGCGA	GTGGGACTTC	7680
TGTTTTGGCA	GGATTACCTG	GAGGCGTTGC	TATGGCAATF	ACCAATCCAG	CTGATGTGSC	7740
TCAATTTTAT	GCTTTCTCTC	TGAAATTGGC	TCAAGAATTA	GGTTATATTT	ATGGTTATGA	7800
GGATCTTTGG	GCTTCAAGAG	AGGAGTTGAG	TGAAGATGCT	CAAAAATACCC	TCTTGCTTTA	7860
TCTAGGCGTA	ATGTTAGGGG	TGAATGGAAC	CGCTGCTTTG	CTACGTGTTG	GTAGTATAAC	7920
AATTGCCAAA	CAGGTAATGA	AAATAGTGCC	TAATAAAGCT	TTAACAAGA	CGCTTTGGA	7980
CCCTATTTTG	AAAAAAGCTT	TAAAAATATT	TGGTGTAAT	CTTACCAAGG	GAGGTTGGC	8040
CAAGGAATG	GGGAAATTTA	TTCTATCTTT	GGGTGGTATC	ATTTACAGTG	GTTTAACTTT	8100
TGCAACTATG	AAACCAATGG	GGGAAGCTT	GCAGAAAGAA	TTATCCAAGC	TAGTCAACTA	8160
TAGTGAAGTT	CAATATCAAG	AGATGTTTGA	AACAATCCGA	AAAGAGGCTG	AAATCATCAA	8220
AGGAGAGTAA	TATGAATCCT	ATCAAAAGCTT	TTGCTAAAAT	TTATGGTAAT	TACTTTTTGA	8280
CGGTGCAAG	TGTAAAAGTG	ATGAAAACGA	TAAAGAAAGC	TGACCATGTC	GTGTTGGTTC	8340
TGGCGAAACT	TTTTATTGCG	GACAAGTTAA	TGGATACGGC	TCGGTGGCTC	ATTAAGCCAG	8400

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AGGAGAGAGA ATGAAATTTT TTGGTCTTC TTGCTATTC TTTTATCAA CCGATTATC	8460
GGATTGTGAA ATTCTTTTGG ATGATCATCT CTTTGCAGT CCAATTGCTG TTTTACAAGA	8520
TAGTGTTTAA GATATTGGAT TGGCTCTTA AACTPATCTA GATGGTAATC CAAGTTGCAG	8580
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CAGTAAATC ATTATTACT CTCTGAAAT CTCTTCAAC CACGTGAGT TCACCTTGCA	8700
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TACGCACACT GGAAGCGAAT GGCTACGAAG TGATTGGATT AGACTAATGA CAGATGAACG	9120
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TCAAGATCGC TTTGATGCGA CCTTACGGG CGTCTAGCC ATCGAGATT CCCTTATGGA	9240
GCACGAGCTG ATGAACCTCG ATTCCGGCGT CACTTTTGAA GATGTTATGG AACTCTGTGA	9300
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TCCAGGTCAC CCAGTTCTGT TCTTCAAGA AGAAATCTG GCTCTCCGTG CGGCTTGAT	9420
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GATGCGTAAG GGTTTGTGTC GTGAGTGGG ACTTGTGGT CAATTGACA TCCATTACCA	9540
ACGTAAGGAA GAACTCTCTT TTCTATCAT GGAGCGCTAT GGACAGATT CACCTCCCAA	9600
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CAAGTCACTA CCAGAGTGT CAATTAGCAG GTTAAAGGAA GCTTTTGAAG CTTTGGCGC	9720
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TAGTCAACAG GCTTTTGGTA ATGGCTATCT TTCAGTCGAG CAGGCCAATC TCATCTCTCA	10080
TCATCTCCCT ATGGAGATTA CCTTTGTCAA TAAAGAAGAT ATTTCCAGT ATTACAATGA	10140

1206

CAATACGCCA GCTGATGAGA TGATTTTCAA ACGGACGCCG TCCCAAGTCG GCGCAATGT	10200
CGAATCTGCG CATCCGCCCTA AGTACTTGGA CAAGGTCAAA ACTATCATGA AGGGGCTTCG	10260
TGAGGGAGCG AAGACAAGT ATGAATGTG GTTCAAGTCT GAGTCGCGAG GTAAGTTTGT	10320
CCACATCACC TATGCTGCAG TACACGATGA AGACGAGAA TTCCAAGGAG TGTGGAGTA	10380
TGATTCAGGAT ATCCAGCCCT ACCGTGAGAT TGATACGGAC TATTTTCGTG GATTAGAATA	10440
AGGAGAAAAA ATGAGTTACG AACAAGAATT TATGAAGGAA TTGAAGCTT GGTCAATAC	10500
CCTAATCATG ATTAACGACA TGGCGCACAA GGAAAGCCAA AAGCTTTACG AAGAAGACCA	10560
GGACGAGCGT GCCAAGATG CCATGATTCG CTACGAGAGT CGCTTGGATG CTTATCAGTT	10620
CTTGCTTGCT AAGTTTGAAA ACTTCAAGT AGGCAAGGGA TTCCATGATT TGCCAGAAGG	10680
CTTGTTTGCT GAGCGAATT ATTAACGAG AAAGATTCTT GATTTTTCAC TAAAATCTTG	10740
ATAGAATGTT TATGTTAAAT CCTTGTCAGA GCAGGGAATT TTTATTGAAA GGATTTTATC	10800
ATGTCAAAGA AACTCAATCG TAAAAACAA TTACGMAATG GCCTCCGTCG CGCAGGTGCC	10860
TTTTCAGTA CGGTACTAA GGTGTAGAT GAGACAAAAA AAGTCGTGAA CGGTGCAGAA	10920
CAGTCAGCAA GCGCAGCTGG TAAGGCTGTT TCTAAAAAAG TTGAACAAGC AGTAGAAGCT	10980
ACCAAAGAGC AAGCTCAAAA AGTAGCTAAT TCTGTAGAAG ATTTTGCAGC AAATTTGGGT	11040
GGATCTCCAC TTGATCGTGC CAAGACTTTC TATGATGAAG GAATCAAGTC TGCTTCAGAT	11100
TTCAAAAACCT GGACTGAAAA AGAACTCCTT GCCTGAAAG GAATCGGCC AGCTACCATC	11160
AAGAAATTGA AAGAAATGG CATCAAGTTC AAGTAATTTT TCTTGAGCCT TGCATTTCCG	11220
AAAAAACTCT GCTACAATAG AGCCATTAGA GGTGTTTGA ATCCACATT TTACAGAAAG	11280
TGGCGGCGCT GAGAAGTCCA CAAATGTGTC AAAACTGGTT GCTAATGGAT GAAAAATTGA	11340
AATAAAAGTG TCTTTTGTCT TTAAGACGA GAGTTGCG	11378

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

CCGCGAGCCA CGGCGAATT GCTGCGGGA TTCATCAGTC AGGATCTATG ATCTTTGGTG	60
AACAAGAAAA GGTTCAGTT GTGACCTTTA TGCCAAATGA AGGTCTCGAT GATCTATACG	120
CTAAGTTTAA TAACGCTGTT GCTGCATTG AOCGAGAAGA TGAGGTCTTA GTTTTGGCTG	180

1207

ACCTTTGGAG TGGTCTCCA TTAAACCAAG CTAGTCCGCT GATGGGAGAA AATCTGAGC	240
GTAAGTTTGC CATCATCACA GGACTTAACT TACCGATGTT GATTCAAGCC TACACAGAGC	300
GCCTCATGGA CGCTCTGCA GGTGTAGAAA AAGTCGCTGC TAATATCATT AAAGAAGCCA	360
AAGATGGCAT CAAAGCTCTT CCAGAAGAGC TAAATCCAGT CGAAGAAGTT GCAAGCGCTG	420
CAGCTGCTCC AGTTGCCCAA ACTGCTATCC CAGAAGGAAC TGTTATCGGA GACGTAATA	480
TGAAATCAA TCTTGCCCGT CTGACACAC GTCTACTTCA CGGTCAGGTT GCAACTGCTT	540
GGACTCCAGA TTCAAAAGCA AATCGTATCA TCGTTGCTTC AGATAACGTT GCTAAAGAGC	600
ACCTTCGTAA AGAATTGATT AAACAAGCAG CTCGAGGTAA TGTCAAGGCT AACGTGGTTC	660
CAATTCAAAA ACTGATTGAG ATTTCAAAG ACCCACGTTT TGGAGAAACA CATGCCCTTA	720
TCTTGTTTGA AACACCTCA GATGCCCTTC GTGCCATCGA AGGCGGCGTG CCAATCAAGA	780
CTCTTAATGT TGGTCTATG GCTCACTCAA CAGGTAAAC ATTGCTCAAT ACCGTTTTGT	840
CTATGGACAA AGAAGACGTT GCTACATTTG AAAAAATGCG TGACTTGGGT GTTGAATTTG	900
ATGTCGGTAA AGTACCAAAAT GATTCTAAAA AAGATTTGTT TGACTTGATT AACAAAGCCA	960
ATGTCARAATA AGCCATTATT TATGAAGGA TTTTAAACAT GTCTATTATT TCTATGGTTT	1020
TAGTAGTCGT TGTAGCCTTC TTTCGAGTTC TTGAAGGCAT CCTCGACCAG TTCCAATTTT	1080
ACCAACCACT TGTAGCCTGT ACCCTTATTG GCTTGTAAAC AGGTCACTTG GAAGCAGGGA	1140
TTATCTCTGG TGGATCGCTT CAAATGATTG CCGTTGGTTG GTCAAAATATC GGTGCTGCTA	1200
TCGCTCTGTA TGCTGCACTT GCTTCTGTG CTGCTGCCAT TATCATGGTT CTTGGTGGTG	1260
ACTTTACCAA GACTGGTATC GGTGTTGCC AAGCGGTTC TATCCCTCTT GCTGTAGCTG	1320
GACTTTTCTT GACAATGATT GTTCGTACAA TTTCAGTTGG TTTGGTTTAT ACTGCAGATG	1380
CTGCCGCTAA AAAAGGTGAC TTCGGCGCTG TGGAGCGTGC GCATTTTCAT CGGCTACTTT	1440
TCCAAGGACT TCGTATCGCG CTTCCTGCAG CTCTCTCTCT TATGGTACCA ACTGAACTG	1500
TACAAAGTAT CCTTACTGCC ATGCCAGACT GGCTCAAAGA TGGTATGGCT ATCGTGGTG	1560
GTATGGTCTG TCGCGTTGGT TACGCCATGG TTATCAACAT GATGGCAACT CGTGAAGTAT	1620
GGCCATTTCT CGCTCTTGGT TTGTTCTCTG CTGCTGTGTC AGATATTACT CTAATCGGAT	1680
TGGTGCTAT CGGCGTTGCT ATCGCTCTTA TCTACCTTCA CCTTCTAAA ACTGGTGGAA	1740
ATGGTGGCGG AGGAGCCGCA ACTTCTAAGC ACCCAATCGG CGATATCTCA GAAGACTACT	1800
AAGATAAGAA AGGACTGAAA ACATCATGAC TGAAAAACTT CAATTAACTA AATCAGATCG	1860
TAAAAAAGTT TGGTGGCGTT CAACCTTCTT ACAAGGGTCT TGGAACTTTG AACGGATGCA	1920

1208

AAACTTGGG	TGGGCTTATA	CACTCATTC	AGCTATCAAA	AAACTCTATA	CTAAAAAGA	1980
AGATCAAAATC	GCTGCTCTTG	AGCGTCACCT	TGAGTTCTTC	AACACTCAATC	CATACGTAGC	2040
TGCTCCAGTC	ATGGGGGTTA	CTCTTCCGCT	TGAAGAAGAA	CGTCTAAAG	GTGTGGAAT	2100
CGATGACGCT	GCTATCCAAG	GGGTFAAAAT	CGGTATGATG	GGACCTCTTG	CTGGTATCGG	2160
TGACCCAGTA	TTCTGGTTTA	CAGTACGCTC	AATCTTTGGA	TCTCTCGGTG	CTTCACTTGC	2220
CCTTACTGGC	AATATCTTGG	GGCCACTCCT	CTTCTTTGTT	GCATGGAACT	TGATTCGTAT	2280
GTCACTCTTG	TGGTATGTTT	AAGAGATTGG	ATACAMGGCT	GGATCAGAAA	TCACTAAAGA	2340
TATGTCGTGT	GGTATCCTTC	AAGATATCAC	TAAAGGAGCT	TCTATCCTTG	GGATGTTCAAT	2400
TCTTGCTGTG	CTGTGTTCAAC	GCTGGGTAAA	TATTAAATTT	GCTTTTGGATG	TTTCTAAAGT	2460
TCAACTAGAT	GAAAAGGCTT	ATATCCATTG	GGATAAATTG	CCAGAAAGGT	CTAAAGGTAT	2520
CCAAGAAGCA	TTCCGACAAG	TAGGACAAGG	ATTGTCTCAA	ACTCCGAAA	AAGTTACTAC	2580
TTTCCAACAA	AACTTGAGTA	TGTTGATTCC	TGGATTATCA	GGACTACTCC	TTACTTTTACT	2640
TTGCATGTAC	TTACTTAAGA	AAAAAGTATC	TCCAATCACT	ATTATCCTTG	CCCTCTTCCG	2700
AGTGGGTATT	GTGGCACATG	TTCTTCACAT	CATGTAAATCA	AGCAACTAAA	AAGGAACAG	2760
GTTCFAAAAT	CTGATTCCTT	TTTTCTATGC	TTTTATTTCAG	CCAAGGCTCC	CATTGGATCC	2820
CATGTTGCAA	GTACGATTGG	TTCTGCTCCA	TAGGCAGCTT	GTTCCTTCTGC	TGTCAAGCAAT	2880
TCCTTACGAA	CAACGATTGG	GTATGTGTAT	TGCTCCATCC	AAGCGTCTGA	GGCAACAAG	2940
TAAACATCTG	TACCGACCTT	GTCTCCCAT	GAGTTTCAA	CTTCCACTTT	GGTTGATTTA	3000
CCATTTTTGT	CCAAGTCAAC	ACCTGTCAAG	ACCATGGCGT	GGGTGATCAA	GCTTTTACTA	3060
TAGTCCAAAC	GTCCAGCCTT	GTCTTGAGTA	AGTTTAATGT	CCATGCTTGA	TTCAAAATCA	3120
TAAACATCTG	TCCGAAGGAT	GCCAGCTTAC	GGTTGCTGAG	CTGCCCGACA	TCAGAAACAA	3180
ACCAACAGAT	CTCACCTGCT	TGCATTTGGG	CAATCGCCAA	TCTTTTCAAG	CGCTCCATTG	3240
GAACGTTGAT	GTAGCGAACT	GCACGGCTAC	CAACCCACAT	CCCCAACATC	TCAACTGTGT	3300
AAGATTTTCC	GTAAGGTTTA	TCAGCAGTTG	GAGCATTTGAT	AACAGAAACG	TAGTCTTCTA	3360
AAGGAAGATT	GACATATTTT	TTGTAAAACT	CTTGTGGTGT	GATTCCTTTT	TCACTTTGTG	3420
AGTTGTTTAT	TTTATTCGGA	TAAACAAAGT	CAAACTTGGG	TGGTGAAGT	CCTAATGACA	3480
TAGCAAGAAA	GTAAAGATT	TCTTGCAAGA	GGTCTCTTTT	CTTAGCTTGA	ACAGTCCCTT	3540
GATCTGACCC	AGAAACAAGC	AAGTCACGCA	AGATTGAGC	ATCTTGACGA	AGCAATTTAT	3600
TAAAGGATGCG	ATTTAGCTCA	CGACTGCTGC	TAGATGAAAC	AGACTCAGGA	TAAACTGACT	3660
TAGGCACGAC	ACCGTATTTT	TCAAAGAGGG	AAACGACCAT	ATCCCATTTGA	CCGCCATCTT	3720

1209

GTGAGGTGT TTGAGTAAG AAGCTAACLT GCGCTAGTCT AATCTTGGT CTGAAGTCGC	3780
AATGACTTGC TCCAAGAACC AGTTTGATTI CTCATACTTA TCCCAGAAGA AAGTGTGGGC	3840
TTGTGACAAC TCAAGTTTCT CCAATTTGTA TTGCGAGATG AGTTTGTGGC GGAAGGTGTT	3900
GAGAGCCGCA AACATCCAGC AACGACNAGA CGTTTCTGG TTAGTGACCT TGTCTTGGT	3960
TAAATCCAAT GAGAAACAG GTGTGTTGTC TACATGGCTT TGGCGACGTT CCAGAGCTGC	4020
AAAAATCCG TTGTGGCTGG CAGCATTTC AATCGCTTGG TATTTTACAT TTGCTTCATA	4080
GTGGCAAAAT AGTTTATCAG TAAATGATTC TTGAATCGCG TTCAATGATT CCTCTTTTA	4140
GTCTACAGTG TATTGG	4156

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3902 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

AAAAACAACA AATAAAACA AAAACAAAAA TATCGAGGTT TATTTTCAAA ACTTTCGATA	60
TTTTATTAA GTATTATTT TGTGTTTCT AGTTTACTTT TTGATGGTTA AGAGTGGTGG	120
AGAAATATAC TCAATGAAAA TCAAGAAGCA AACTAGGAAG CTAGCCGACG CCGTACTTGG	180
AGTAGCGCAA GCGCAAGCTG ACGTGGTTTG AATTTGATTT TCGAAGAGTA TTAGTGCAAA	240
CCGTAGTTGT AGTCATCATC TTGCATGGCT TCAACTTCGC CAAGAAGGTA ACCATTTCGG	300
ACTTGAGAGA AGAAGTCATG GTTGAAGTTT CCTGTTGAAA TACCGTTTCAAT AACGATTGGG	360
TTGACATCTT CAGCTGAATC TGGGAAAAAG GGATCTTGT CCAATGTTTCAAT GAGAGCTTTA	420
TTGGCAATGT AGCGAAGGAA GTTTTTAAAC TCTTCAGTCC AACCACACCC GTCATAAAGA	480
CTCTCTGTGT AGCCTTCTTC ATTTTCATAA AGAGTATAGA GTAGTTCGTA CATCCATTCT	540
TTGAATTTTT CTGCTCTTC TTCAGGTAAT TCATTGAAAC CAAGTTGGAA TTTGTAACCA	600
ATGTAGGTTT CGTGAACAGA CTCGTACGGA ATATCAATT TAATGATTTT TGCAACGTTG	660
GCAAGTTTGT TGTACCGAG ATAGTAGAGG GGAGTGAAGA AACCAAGATA GAAGAGGAAG	720
GTTCGAGGA AGACGCTGGC AACTTTCCTT TCAAGTGGGC TGCGGTTTAG GTAGATTTCG	780
TTGACAAATC CAGCCTTCTT TTGTAGGTAA GGATTGGTAT TGGTCCATTC GAAATTTTCT	840
TCAATCTCAG CCTTAGTATT CAAGGTAGAA AAGATTGATG AGTAAGATTT AGCGTGGACA	900

1210

GATTCACATAA	ATGGGATGTT	ATTGAAGACA	GCTTCCTCAT	GTGGTGTAAG	GATGCTGCG	960
CGAAGGGCTTT	GAACCCAGT	TTTCAGATTGC	ATAGTGTCAA	GAAGGGTTAA	ACCACCAAAA	1020
ACTTTTCCGA	CCAAGTCTTT	CTCTTTGTTA	GATAGCTTTC	TCCAGTCATC	CAAGTCGTTT	1080
GATAAGGGAA	TACGTGTATC	GAGCCAAAAT	TGCTCCGTCA	GTTTTTCCCA	AGTTGATTTC	1140
TCCATAGACAT	CTTCGATGGC	ATTCCAGTTA	ATGGCTTTGT	AGTAAGTTTC	CATTTAAAAAT	1200
CTCTTTCGT	GTTCAGTATT	GCGAATCAC	AATTATTTC	ACTTTACCAT	AATCTATAG	1260
GAGTATCCGA	CAAAAAGTCG	GAAGCCCGAC	TTTAAAAATG	TTACATAAAT	TATGTTATGA	1320
CATAGTAGAT	TTGATTTTAT	CAGTGCTGCT	TAGGGAATAA	TAGTGTTCCT	ATGCTAGAAA	1380
CTAAATCACA	CAGCTTTCAC	ATTGGTTGGC	GCCGACTTCT	CCACCGTCAT	CTGTAAAGGT	1440
ACGGACGTAG	TAGATAGACT	TGATTCCCTT	GTAAAGGCA	TAGTTACGAA	GGATGGACAA	1500
GTACAGTGTC	GTTCGTTTAT	TTTCCCTCTT	CCATTCGTAA	AGGCCTTTTG	GAATGTCAC	1560
GCCCATGAAG	AGGGTGAAGT	AAAGTCTTTG	ATCCACGTGT	TCAGTCGCAG	CAGCGTAAAC	1620
ATCCATGACT	TTACGCATAT	CCATATCGTA	GGCAGAGTGT	TAGTAAGGAA	TGGTTTCTGT	1680
AGACAAGCCA	GCAGCAGGTT	AATAGATTTT	ACCAATTTTC	TTCTCTTGGC	GTTCCTCGAT	1740
ACGTTCGGTA	ATCGGGTGA	TAGAAGCAGA	AACGTCGTGT	ATATAGCTGA	TAGAACCATT	1800
TGGCGCTACA	GCAAGGCGAT	TTTGGTGGTA	AAGACCATCT	TCTTGAACCT	TGTGCGGAAG	1860
TTCAAGCCAA	TCAGCAACAC	CAGGGATAAA	GACATTTTGT	AAGGTTCTCT	TAACACGGTC	1920
TGATGTTTGA	ACAAATTTCAC	CAGTTACATA	CTTGTCAGAG	TAACTTCCGT	TAGCATAGTC	1980
TGATTTTCCA	AAGTTGTGGA	AGGTAATACC	ACGTTACAGT	GCAATATTGT	TTGACTCTAC	2040
CAAGGTCAG	TAGTTCATAA	GCAATAAGTA	GATGCTTGTA	AATTCAACAG	ACTCAGGTGA	2100
ACCATATTCA	ATGAGTTGTT	GGGCAAGGTA	GCTGTGCACT	CCCATGGCAC	CGAGACCAAA	2160
GGTGTGGGCT	TGGCTATTTC	CATGGTCAAT	CGTTGGTACA	GCTACGATAT	GTGAACATATC	2220
TGTAAAGAAA	GTAAGGGCAC	GAACCATAGC	ACGGATAGAA	GACCCAAAAT	CAGGTGAAGT	2280
CATCATGTGA	ACCACGTTGG	TTGAACCCAG	GTTACATGAA	ACATCTGTTC	CCATTTGAAG	2340
GAATTTCTGA	GCATCGTTGA	TCAAGCTTGG	TTCTTGAAC	TGAAGAACTC	CAGAACACAA	2400
GTATCTCATG	ATAATCTTTC	CATCAACAGG	ATTTCGACGG	TTAGCCGTAT	CGATGTTGAC	2460
TACATAAGGA	TAGCCAGACT	CTTGTTCGAA	TTTAGAGATT	TCAGTTTCCA	AATCCGCGC	2520
CTTGATTTTT	GTCTTCGGA	TATTTGGATT	TGCGACCAAT	TCATCGTATT	TTTCAGTAAT	2580
GTGATGTAA	TTGAATGGCA	CACCGTATTC	TTTTCTTACA	GAGTAAGGGC	TGAAGAGGTA	2640
CATTTCTTCA	TTTTTACGAG	CCAATTTCGTA	GAATTTATCA	GGTACTACAA	CACCAAGTGA	2700

1211

TAGAGTCTTG ACACGACTT TTTTCATCAGC GTTTCCTTTC TTAGTTGAAA GGAAAGCGAT 2760
 GATATCTGGG TGAAAGACGT TGAGGTAGAC AACACCAGCA CCTTGACGTT GCCCAATTG 2820
 GTTGGAGTAA GAGAAGCTGT CTTCAAAAG CTTCATAACA GGAACGACAC CTGAAGCAGC 2880
 TCCTTCATAG CCTTGTAGT GTGCACCAGC TTCACGAAGG TTGCTGAGGG TAATTCCAC 2940
 ACCACCACCA ATACGTGAAA GTTGAAGAGC TGAGTTGATA GAACGCCGA TAGAGTTCAAT 3000
 ATCATCCGTC ACTTGGATTA GGAACAAGA TACCAACTCC CCACGACGAG CAGTCCAGC 3060
 ATTCAAGAAG GAAGGAGTAG CAGGTTGGTA GCGTTGGTGG ATGATTTTCA TGGCAATATC 3120
 GATTGCAACA GCTTCATTCC CATCAGCGAA ATAAAGGGCA TTGAAGAAGA CACGCTCTTC 3180
 CATATTTTCA AGATAGTATT CACCGTCATT AGTCTTAAAG GCATATTGAT TGTAAAATT 3240
 ATAAGCTGCC ATGAATGACT TGAATTGGAA GTTTTGGTCT TTGATAAATT GAGCTAATTC 3300
 TTCCAAGAAC TCTGACGCT ATTTCTTGAT AAAGCTGTT TCGATGTAGT TGTGTTCAAT 3360
 GAGGTAATTG ATTTTGTCTT TGATTGAATC AAAAACCATA GTGTTTGGAA CTACATTTTC 3420
 TTTAAGAAA GCATCCAAGG CTTCCTTGTC TTTATGAAGC ATGATTTGTC CATTAACAGG 3480
 ACGGTTAATT TCGTTATTAA GACGGAAGTA AGTCACGCTC TCAAGATGTT TTAATCCCAT 3540
 AAAATTTTCC TTATCTAATT ACAAAAGAAA GGCTCTAAG TTAGCCCTAA AAGCAGTTTC 3600
 TTCTGGATGA TGTACTAAGA TTATGCTAAT TGTTCAGTT TTCTGCTG GAAACCTGAA 3660
 AAGACTTCAG TTGGTGTTC GATAACAGGA GCTGCGCTAA AACGAGCTC TTTAACTTGA 3720
 TCGACGTACT CAGGTGCTC ATCAAGATTG ATTTACAGAT AAGAGACATT ATTAAGTCC 3780
 AAGAAACGCT TGGTCATTTT ACATTGGACA CAATTGTTTT TAGAATAAAC GGTACCAT 3840
 GTGTAACCC TCTTCAAAAT TTAATACTAT CTTAGTATAT CAGAAAATAA AATTTTGTG 3900
 GG 3902

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2456 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

TATTGAAGCT ATTGTAGACT ACAAGATAA GGATTTGCG TTAGTAGGCG GTGAGACTCA 60
 CTGATAACCT AAAAAGGATA GTCAATTATG CTTGTTTACT AACTATTAACT TAGCTAAAT 120

1212	
CAATTGAGGT TGTTCACATA AAACCTCTATA TCAGAGAAGC CTGATATAGA GTTTTTCCTT	180
GCTAGTTTATA GGATTTTTTT GTAAAAATAGA AAAAGTGAAG AGAGGTATGA AATGAGCAAG	240
AAAGATAAAA AAATCGAAAT TCAAGTAGCG GATGCCAAAG TTAATGTTGG TAAAGACAGT	300
TTTGAAGGTT ATACATTGAC TATCGGTAAA AAAGTATCTG GAGAAATTGC CGAATTAGAC	360
GGACAAATTTG CCATATATAA GAATGGGAAT GTCGATAGTT TTTATAAAAA APTGGAAAAA	420
GCTGTGAAAA TTTTGATTGA AAATATATAA TTAGCAAAAT AAGTCTTGTT TTTTGAAT	480
TTTCATGATA TAATAGTCCA TGTGATTGT AGGAGAGATA GCGAAGAGGC TAAACGGGC	540
GGACTGTAAA TCCGCCCTT CGGGTTCGGT GGTTCGAATC CCTCTCTCTC CATTTCAATTA	600
ATGGGGTATA GCCAAGCGGT AAGGCAAGGG ACTTTGACTC CCTCATGCGT TGGTTCGAAT	660
CCAGCTACCC CAGTCTCTAG GTAAATATCA AGATAGAAAG CAAAATATCT TAGGGTATTT	720
TATTTTTATA ATTGAAGAC GTGAATGATA TGAACATGTC CTTGCGGGTG CTTAGGAAAA	780
AAATTATAAG TATGTCAAAT TTAAGAAAAA CTTGATTTGT GAGGATTTT TTAGATGAAC	840
GAATTTGAAG ATTGTCTAAA TAGCGTAGT CAAGTTGAGA CTGGTGATGT TGTAGTGCT	900
GAAGTATTGA CAGTTGATGC GACTCAAGCT AACGTTGCAA TCTCTGGAAC TGGTGTGAA	960
GGTGTCTTGA CTCCTCGCA ATTGACAAAC GATCGTGATG CAGATATCAA TGACTTTGTT	1020
AAAGTAGGAG AAGTATTGGA TGTCTTGTA CTTCGTCAAG TAGTTGGTAA AGATACTGAT	1080
ACAGTTACAT ACCTGTGATC TAAAAAACGC CTTGAAGCTC GCAAAGCATG GGACAAACTT	1140
GTTCGTGCGC AAGAAGAGT TGTACTGTT AAAGGAAGCG GTGCCGTAA AGGTGGACTT	1200
TCAGTAGAAT TTGAAGGTGT TCGTGGATT ATCCAGCTT CAATGTTGGA TACTCGTTTC	1260
GTACGTAAAC CTGAGCGTTC TGTAGGTCAA GAATTTGATA CTAAATCAA AGAAGTTAAC	1320
GCTAAAGAAA ACCGCTTCAT CCTTCAAGT CGTGAAGTTG TTGAAGCAGC TACTGCAGCA	1380
GCTCGCGCTG AAGTATTCGG TAAATGCGT GTTGGTGATG TTGTAACCTG TAAAGTTGCT	1440
CGTATACCAA GCTTCGGCGC TTTCTGCGAC CTTGGTGGTG TTGACGGATT GGTTCACCTG	1500
ACTGAATTGT CACATGAACG TAATGTATCA CCAAAATCAG TTGTAACCTG TGGTGAAGAA	1560
ATTGAAGTGA AAATCCTTGA TCTTAAACGAA GAAGAAGGAC GTGTATCACT TTCACTTAAA	1620
GCAACAGTAC CAGGACCATG GGATGGCGTT GAGCAAAAAT TGGCTAAAGG TGAATGATGA	1680
GAAAGAACAG TTAACCGTTT GACTGACTTC GGTGCATTTG TTGAAGTATC GCCAGGTATC	1740
GATGACTTGT TTACAGTATC ACAAATTTCA CACAAACGGA TTGAAAAATC AAAAGAGCT	1800
CTTAAGATTG GTCAAGAGT TCAAGTTAAA GTTCTTGAAG TTAACGCAGA TGCAGAACGC	1860
GTGTACCTTT CTATTAAAGC TCTTGAAGAA CGTCCAGCCC AAGAAGAGG ACAAAGAGAA	1920

1213

GAAAAACGTG	CTGCTCGTCC	ACGTCGTCCA	AGACGTCAAG	AAAAGCGTGA	TTTCGAACTT	1980
CCAGAAACAC	AAACAGGATT	TTCAATGGCT	GATTGTGTTG	GTGATATCGA	ACTTTAATCA	2040
AATTGAAAAA	TCACAAAATC	CTTTGTTTAC	TAAACAAGGG	ATTTTCTCGG	CTCTTTGTCA	2100
ACTGTATGTG	GTGGAAGAAA	AGCTAAGCTC	GAGAAAGGAC	AAATTTTGTG	CTTTCTTTTT	2160
TGATATTTCAG	AGCGATAAAA	ATCCGTTTTT	TGAAGTTTTT	AAAGTTCGGA	AAACCAAAGG	2220
CATTGCGCTT	GATAAGTTTG	ATGAGATTAT	TGGTCGCTTC	CAGTTGCGCG	TTAGAATAGT	2280
CTAGTTGAAG	GGTGTTGACA	AGCTTTTCTT	TATCTTTGAG	GAAGGTTTFA	AAGACAGTCT	2340
GAAAAATAGG	ATGAACCTGC	TTAAGATTGT	CCTCAATAAG	TCCGAAAAAT	TTCTCCGGTT	2400
CCTTATTCTG	AAAGTGAAAC	AGCAAGAGTT	GATAGAGCTG	ATAGTGGTCT	TTCAGG	2456

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10974 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AAATAGGATA	TAGAGACATC	CTTCTGATCT	GCTTTTACA	AAGTCCAATT	ATATCGGGAT	60
CTATACCTCC	ACAATGTCCA	TTATTATMCC	TAACATAAAT	ATGAGCCGAA	AACACATATAT	120
CCTTAATGTC	TCCATATCCA	TCAGGGATAT	TAATATTTAT	TTTTCCACAA	CTATATTGCA	180
TTGTAAACAT	CTCCTTAAAC	GACGCAATTAT	GATATTGTAT	AGAGAAATTT	TTATGAATAA	240
CTCAATTAAT	TTATAGTAAA	TCATGCTTAT	ATCTCAAAAG	TACCTATTTT	ATCTTGCTCT	300
GACCTTCTCC	AAAGAAATGC	TATAATACTA	TTACAAATCC	ATCTGCACATA	CACCTCAAAAT	360
TTTAGACACTG	TATAAAAACG	TTTCAATACA	CTAACCTCAA	GAAAACCTCC	ACTATTAAAT	420
GAAAAAATTG	ATAGAGATAA	ATTAAAAATC	TATATTGAJA	CTCATCCCGA	TGCTTATTTG	480
ACTGAAATAG	CTGCTGAATT	CAACTGTCTCT	CCAACAACFA	TTTATTACGC	TCTAAAGGCT	540
ATGGGATATA	GTCTAAAAAA	GAGCCGTACC	TACTGGGAAC	AAGACCCAGA	AAAAGTAAAT	600
CGGTTCCCTTA	AAGAACTGAA	TCACTTAAAG	TACCTGACTC	CTATTTATAT	TTATGAGACA	660
GGGGTTGAGA	CCATTTTTTA	TCTCGAATAT	GATCGAGCCT	TGAGCAGGCA	GTTAGTCTCT	720
CTGGAGAAG	ATATAATTAT	TTGAATTAAAG	ATCGAGACAA	CGCACACCAG	AGATTGCGAT	780
ACTGTTATAG	AAGTACTAAT	GCCTTTTTTT	GTTTCAATAT	ACTATGGCTC	CGATGACCTA	840

1214

TAAAGATACG ATGACGAGTG ACTTTTTCGA AGCTTGCTTC CAAAAATTCT TACTACCTAC	900
TTTAGATACA CCATCCCTTA TCATTATGGA CAATGCAAGG TTTCACAGAA TGAACATGTG	960
TAAGGAGCAG GGCATAGACT GTTACCACTT CCTACTTATT CACCCGAGTA TAATCCCATTT	1020
GAGAAATAT GGGCTTACAT CAAAACATC TCAGAAATAT ATTGTCAAT TACGATGCTT	1080
TTCTTTGAGGC ACTTTTGTC TATTCTGTG TCAGCCGACT ATACTCCGTT ATTGGGCAGC	1140
TACGGAACAG TCGATGGGAC GATGGGGGA CATAAAAAA TCCTCCAGTT TTGTTTTTTA	1200
TAACAGTATA CTGGAGAAAT GACAATCTCG GTAGATACCT CGTTATAGCG CGGTTACTTA	1260
TTAGGCAGTT ACAAACAAC TGTGAACAGA AAACATTCCA GAGTCAGACA AGACTTTGGA	1320
ATGTTTTTGGC TCTATAATTT CTGTAGTGGG TAATCCACCC CCAGGAATTA TAGGGTCGTT	1380
TCTTGTAAGAA AAAAAGCCCC ATATGACCTA TAATGAAGAG CGTCTAACCA ACTCATTAGA	1440
AAGGGTTTCA TTGGAACAAC TTAAGAATAC CACAGATTGG CTCGGATTGG AAGCAAAAA	1500
TATCAAAATC TTCTCTGTTC TGAATATCCA AACCCATCTA GTCCGTTGAG CAAAGTTGGA	1560
TTCCCCCGCT CCTCTTGTG CTCATTGTCA AGGGAAAGTG ATCAAAATAG ACTTCCAGAA	1620
AGCCTCTAAA ATTCCGCTTC TCGACTGTCA GGGTTTACCC ACGGTACTGC ATCTCAAAAA	1680
GGCCCGCTTT CAGTGCAAGA ATTGCCTTAA GGTGGTGTGT TCTCAAAAT CCATTGTCAA	1740
GAAAAATTGC CAGATTTCCA ACATGGTGAG ACAAATAATC GCTCAGCTCC TCCTTGAAAA	1800
GCAGTCTATG ACTGAGATTG CCCACAGATT GGGGGTCTCA ACTTCCACCG TCATCCGAAA	1860
ACTGAGGGAA TTTAAGTTTG AAACCGATTG GACCAAGTTG CCAAAAGTTA TGAGTTGGGA	1920
TGAGTATAGC TTCAAAAAGA GCAAAATGAG CTTCATTGCC CAAGATTTTG AGTCCAAATC	1980
CATCCTCGCA ATTTTATAGC GCGAACTCA TCGGGTGTAT CGAAACCATT TCCAACGCTA	2040
TCAGAGAGAG GTTCGGGAGC TGGTCGAGGT CATCACCATG GACATGTACA GCCCTTATTA	2100
TCGGCTCGCT AAGCAACTCT TTCCAAAGGC GAAGATTGTT CTGACCGCT TCCACATTGT	2160
CAACATCTG AGCCGAGCTA TGAACCGAGT ACGAATCCAA ATCATGAACC AATTGACCG	2220
AAATCCTTG GAGTATCGGG CGCTCAAGCG CTTTTGGAAC CTCGCTTTT TCGTTCTAG	2280
GCTCGGGCTA AATCAGTCCA CTGGACTGAT TTACTACACC AGTATAGCTT CAAGTCTGT	2340
CAGAAACGAT TCTATCAGCC CACGTTTCGA ATGCACTTAA CCATCGGGA AGTACGAGAT	2400
AAGCTGCTTT CTACTCTGA GGGATTACAG GTTCACTACG AACCTCTACA ACTCCTGCTC	2460
TTTCATTTTC AAGAGAAGAA TGCCGACCAT TTCTTTGGAT TGATTGAGCA AGAAGTGCCA	2520
ACGGTTCATC CGCTTTTTC AACGGTCTTT TGGAATTTT TAAGGGATAG AGATTAAGATT	2580
ATCAACGCAC TTAAGCTGCC TTATTCACAC GCTAAACTTG AAGCGACCAA TAATTTCAAT	2640

1215

AAGATTATCA AGCGCAAAGC CTTTGGTTTC CGGAACCTTA ACAATTTTAA AAAACGGATT	2700
TTGATGACTT TGAACATCAA AAAAGAGAGT ACGAATTTTC TACTTCCAG ATTGCAGCTT	2760
TTCCCTTACC CACTACACTT GACAAAGAGC CACTCTTTAT TCCATGGTAT CAAAGGCAAG	2820
ACTTGGTTTG GCATTGAGGT CCCAGCCTGC GAAGTTTCTT TTGTTCCACT CGCTGACGCT	2880
GGCATAGSCA ATCATACCTG CATTTCTTCC GCAGAGTCGC AGAGGGGGGA TGATAACCTT	2940
GACATCTGTG ATTTGGGCTG CTAGGCGTTC TCTGAGACTT TTATTTGGCTG CCACACCACC	3000
TGCCACAACCT AGGATTTTAA CAGGATATTT CTCCTAAAGC TTCTTTGGTT TTGCCATGAG	3060
AATGTCACATA ACTGTGCTT GGAAGGAGC ACACAATCT TCTGTAGACA GGCTTTCTCC	3120
CTTTTGTCTG GCATTTGTGA GAAGATTGAT AAAGSCAGAT TTCAAACCTG AGAAGGAGAA	3180
CTCCAGATTA TCTTCTTAA TCATGGCAGC GGGGAAATCA TAAATATCTT GCCCTGTATG	3240
AGCCAGCTCG TCAATCTCAC GACCTGCAGC ATAGGTCAAG CCCATGACAC GCTCCGACCTT	3300
ATCATAAAGC TCACCAACCG CATCATCAGC GGTTCCTCCA ACAATCTTAT AATCTCTGCT	3360
CTCCGAACA TAAACAACCT CTGTGTCTCC GCCGTGACC AAGAGGGCTA GCAAGGGA	3420
CTCCAAAGGC TCCACACTCT GAGCTGCCAT GAGGTGCCCA GCCATGTGAT TAACAGGAAT	3480
CAGTGGAAAT CCGTGAGCCC AAGCAAAGGC CTTGGCAGCT GACAAACCAA CTAGCAAGGC	3540
TCGACCAAG CCGTGTCTCT AGGTAAACGC AACAGCTGTC ACGTCTCTCT CGTAAATCCC	3600
TGCTTCTGCC AATGCCCTCT CGATACAGGC TGTAAAGACC TCGACATGGT GAGGACTGSC	3660
TACTTCCGGC ACTACGCCAC CAAAACGTTT GTGACTCTCA ATTTGACTAG CAATGACATT	3720
GGACAAGAGC TCATGCTGCT TTTTCAAGAC GCGGACACTG GTCTCATCAC AGGATGTCTC	3780
AAATGCTAAA ATATATCTAT CTTTCATCTA TTTCTCTCTT CATGATAATG GCGTCTCTGA	3840
CTGGTTCATG GTAGTAGGCC TTTGCTCAG CGATAACTGT CATCTTTTCT TTCTTGTAAA	3900
ATGCTTGGCC TCGTTGATTT GACTGTCTGA CTTGAGGAA AATTTCTTTG TCTGTGCGCA	3960
ATTGAGCAA CAAGGCTGAC GCAATCCCTT GACCCTGATA AGTCTCTTG ACAGCGATTT	4020
GCAAGGCTTC TGCTTCAAAA AGATTCTCTT GCACAGCTAG AAATCCAATC ACTTCTGCC	4080
CATCATAGC CAATGCATAC CAAGTCTGGT CTGGGACAG ATCTGCTTGG ATTTGCTCCA	4140
GAGTCAAGG ACTGACTAGG TAAACAGCTG CCAATAACAG GTAGATGGCT TGAGCTAGGT	4200
CAGGCTGTTG TTGAATTGCG TTGATTTCTA TCATAGGCGT TTAATGTAAG ACTCGCCAGA	4260
CTCGGTATGG TTCTTGAGCC AGTTTTCCTC AGCCTGACTG CGTTTGAAGT AATTGCGCAC	4320
AAATCATGCG AAGGAGCTCG CTTCCTTTGT CCAGGCCAAA AGAGCTAGAT TAGCTGCATT	4380

1216

GGGCAATGTT TCTTTGTAAT CAGTCCTTGG CAAGTGTTTT TGAATCTGCT CAACAAAGGG	4440
GCCAACTTCT CCAGCAAAGG TTACCTGACT AGTACCCCTG ACTTTTCTTA GCACCTCTTC	4500
AAAAGATAGG TGCCTTCTG CCATGACAGG TTTCGCATTT TCATAAAATC CTGCATAAAC	4560
ATTATTGCGA CGCGCATCCA TCAAGGGGAC AAACAAACCT TCTTTTGTAT GGGGCACCAG	4620
AGCCCAAGAG CTCGACATAC CAACCAACT GTGTTCAGG GTGTGAGCTA AGGTCTTAGC	4680
AGTTGCTACC GCAATTGCA AGCCTGTATA GGTACCCGGC CCTTCAGCTA CCAAGATTGG	4740
GTCCAAATCC TTGGGTGTCC ATTCCAAATC TGCCATCAAA AAATCGATGG CAGGCATAAG	4800
AGTAATAGTC TGATTTTCT TAATATTAAT CGTCGTCTCG GCAAGAACCT GCTTATCCTC	4860
TAAAAATAGC AGAGAAAGAG CCTTGTGGA CGTATCAAAA GCTAATACCT TCATAACACA	4920
TTCCTATCTT TTGTCTGCT TACTATTATA CTACAAAAGC TGGCACATGG GAATTTCTCT	4980
TGCCCCCAAG CAAGAGTGCC CTCACCTTAAC TAAAAATAAT TAAAAAAAT GCTCACTTTT	5040
CCTTTCTCTT TCCGATAATA AAAGTGAACA AGAAAAAGG AGGAAGGTC AATGCAAAAT	5100
TTTGACATTC TTGACAAATCA ATTTTATCC TTATCTGAAA ATGAATTATC AGATATTGAT	5160
GGCGGTCTCG CTCCTTGGT TATCTTTGGA GTAGCAGTAT CTGGGAAGGC TATTGCAGGT	5220
GGAACAGCAC TTATAGGTTT TGGTTTGGCA GCTGGTTATT TTTTAGGAGG AGATTAAAT	5280
GATGAAGAT TTGAACAATT ATCGTGAAT TTCTAATAAG GAATTGCAAG AAATCAAGGG	5340
TGGCTTTGGT GTCGGTGTTG GTATCGCTTT ATTTATGGCA GGTTATACCA TTGGAAAAGA	5400
CCTTCGTAAA AAGTTTGGTA AGTCATGCTA GATAAGAAAC ACATTTTATG AAGGATAAAT	5460
TTTATTGTCT TCATCTCTTA CAGTTTGCTC AGCATTTCTA ATGATTGAA CATTACTACC	5520
ATCCCTTAC CATTCGATTT ATCTGTTTGT ATTTGTTTAT TTTTATGCTT CAACTCTATT	5580
TTTGATCAGA ACAATGACTC CCATAAAAAT AATAAGCTTT GAAAATTCCA TTGTATGTC	5640
ATGTTAGAAA AATGCAAGA CCACCTCATC TTGATAGATG GGTGGGAATT TTCGTGCTG	5700
AAATCTACTA TCTCTACATT CCCAAACAAA AAACCCAGC ATAAGCAGGG CATCTAAGCA	5760
TTTAATTCAA AGTAAAAATC AAACCAAGC ACATAGGTCA CGAGGAGAG AAAAAGCGAG	5820
TAGAGAGTCA CAAAGGTCTT TTTCACAGG AACTTGGTTT GTCTCGTTTC CAGTTTGGCA	5880
AATGAAAGAT TCCCCGATA AACGCAAGCA CAAAAACAA TAAAGCTAC CAGCGAGCT	5940
CCGATAGCAA AAGCAATAA GTTATACATA GGGCAACCTC CTGACTTAA AATCTATATG	6000
GAATPATGAC AAGCAATAA TTTCACCTCC GTTATCAACA TAATACATTT TCTTATTTT	6060
TGAAAAAGCT TACCAAGAA ATCGTCCCTC AACTTTCTCG TTTCGCTCTT TTACTAAATT	6120
TTCAATTTGT GGTATAATTG AAATAATTGT AACGAATCAA GGTCAATCTA GACACAAAT	6180

1217

GGAATGAAAT	CAAGCAAATA	TCTGCTAAAA	GTTTGGAAAT	AGCTGACCTG	TAAATAGAAA	6240
GGAATATAT	GATTACAAAA	GTTTTPTATC	AAGAAACAAA	AGAACGTAGC	CCACGCCGTG	6300
AAACAAACAG	CACGCTTTAC	CTAGACATCG	ATGCCAGCTC	AGAACTTGAG	GGCCGTATCA	6360
CTGCTGCCCA	ACTTGTGAA	GAAATCGCC	CAGAGTACAA	TATCGAGTAT	ATCGAACTCT	6420
TGTCTGACAA	ATTGCTCGAT	TACGAAAAAG	AACTGGCGC	CTTCGAAATT	ACGGATTTCT	6480
AATATGGCCT	ACACTCTTAA	ACCTGAAGAA	GTCGGCGTTT	TTGCCATCGG	TGGTCTAGGA	6540
GAAATCGGGA	AAAACACTTA	CGGAATTGAA	TACCAAGACG	AGATTATCAT	CGTCGATGCT	6600
GGGATTAAAT	TCCAGAGA	TGACTTGCCT	GGTATCGACT	ATGTCAATCC	TGACTACTCT	6660
TACATCGTGG	ACAATATCGA	CCGCGTCAAG	GCTGTTTTAA	TACACACAGG	ACACGAGGAC	6720
CACATTGGTG	GGATTCGCTT	CCTACTCAAG	CAAGCAAATC	TCCCTATTTA	TGCTGGACCG	6780
CTTGCTTTGG	CTTTGATCCG	TGGAAACTC	GAAGAACACG	GCCTCTTCGG	CAACGCCAAA	6840
CTTTACGAAA	TCAACACAAA	CACCGAGTTG	ACCTTTAAAA	ATCTCAAGGC	AACCTTCTTT	6900
AGAAGCACTC	ACTCTATTCC	AGAGCCTTTG	GGGATTGTCA	TCTCATCC	TCAAGGGA	6960
ATCGTCTGTA	CGGTCGACTT	TAAGTTCGAC	TTTACTTCAG	TTGGAGAAC	TGCGGACTTG	7020
CATCGTATGG	CTGCGCTTGG	TGAAGAGAGC	GTGCTCTGTC	TCCGTCTGA	CTCGACAAAT	7080
GCGAAGTAC	CAACCTTTAC	CAACTCTGAA	AAAGTCGTTG	GTGAGTCCAT	TATGAAGATT	7140
ATCCAAGGTA	TGAAGGACG	TATCATCTTT	GCATCTTTTG	CCTCAAAATAT	CTTCGCTCTC	7200
CAGCAGGCAA	CAGAAGCTGC	TGTTAAGACT	GGACGCAAGA	TTGCGGTCTT	TGTCGTCTCT	7260
ATGGAAAAAG	CCATTGTCAA	CGGAATCGAT	CTTGGCTACA	TCAAGCTCC	TAAGGGAAC	7320
TTTATCGAGC	CAATGAAT	CAAGATTAT	CCTGCAGGAG	AAGTTCTTAT	CCTCTGTACA	7380
GGTAGTCAGG	GTGAGCTAT	GGCAGCCCTC	TCTCGTATCG	CCAACGGAAC	CCACCGTCAA	7440
GTACAATTAC	AACCAGGTGA	TACCGTTATC	TTCTCTCTTA	GTCCCATCCC	TGGAAACACT	7500
ACTAGTGCTCA	ACAGCTGAT	TAACATCATT	TCTGAAGCTG	GTGTCGAAGT	TATCCACGGT	7560
AAAGTGAAACA	ATATCCATAC	ATCTGGACAC	GGTGGTCAGC	AAGAGCAAAA	ACTCATGCTC	7620
TGCTTGATTA	AGCCAAAAATA	CTTCATGCCT	GTCCAGCGTG	AATACCGCAT	GCAAAAAGTC	7680
CACGCTGGAC	TAGCAGTGGA	TACTGGTGTT	GAGAAGGACA	ATATCTTTAT	CATGAGCAAT	7740
GGCGATGTGC	TTGCCCTTAC	TGCTGACTCA	GCTCGTATCG	CAGGTCAFTT	CAACGCCCAA	7800
GATATCTATG	TCGATGGAAA	TCGATCGGT	GAAATGGCG	CAGCTGTCTT	CAAGATCGT	7860
CGGATCTAT	CTGAAGACG	TGTCGTTCTG	GCAGTTGCAA	CTGTTGACTT	CAATTCGAG	7920

1218		
ATGATTCTAT CTGTCACGA CATCTCAGC CGAGGCTTG TCTACATGAG AGAGTCTGGC	7980	
GACTTGATTC GCCAAGCCA GCGTATCCTC TTCAATGCCA TTGATATCGC ACTGAATAAT	8040	
AAGGATGCTA GCGTGCAATC TGTCAATGGT GCCATTGTCA ACGTATATCG CCCCTTCCTC	8100	
TATGAAATA CCGAACGTGA ACCGATCATC ATCCCAGTGA TCCTCACACC AGATGAAGAA	8160	
TAAAGCAGA AAACAGCCCC GTCCTCGAG CTGTTTTTCT CTATGCTTTC TTTTGAGATT	8220	
AAAACCTATA CTCAATGAAA ATCAAAGAGC AAACTAGGAA GCTAGCCGTA GGTTCCTCAA	8280	
AGCACTGCTT TGAGGTGTGA GATAGAACTG ACGAAGTCAG TAGCCATACC TACGCCAAGG	8340	
CGACGTTGAC GCGGTTTGAA GAGATTTTCG AAGAGTATCA ATAAAAATCG AATTCAGACT	8400	
AGAAAGCTAA GCGAAAGCAT AACCTTGAGT AGCTCCCAAT GTTCGGGAAA CTATGGGAGG	8460	
CTGGAGATGA ATCAAAGCCA AGCTTTGAAC TCATTCGTAA GAAGCCGACG ACGTATCATT	8520	
TTGATTTTTG AAGAGTTTTA GAAATACTAC GATTTTTTACC TTCAGATAC ACCATCAAAA	8580	
TAGAAATATC TGCTGGGTTT ACTCCGAAA TACGGCTGGC TTGCCGATG GTTTCGTGAT	8640	
TGATGAGTTT GAACCTCTGA CGGCTTCGG TTGCGATAGA ATCAATGTCA TCCAGTGA	8700	
TATTCGCCGG AATGGGTTT TCTTCCATGC GTTTCATCTT GGCAACCTGG TCCATGGCTT	8760	
TGGAAATATA GCCTTCATAC TTGATTTCTG TTTCATCAAA TTCGATAATC TTGTGATCCA	8820	
AGTCTCTGTC AGCTGGTCCG ATGAAGCCA CCACATCTTG GTAAGAAATC TCTGCACGCG	8880	
GAAAGAAATC CTTCGGCTGC ACTGCATCGG TCAAGGGTTT GAAGCCCATC TCCTCAACCT	8940	
TGGCATTGGT TTCTTGACT GGCTTGAGTT TGATAGTTC TAGGCGCTTC ATCTCATTTT	9000	
CAAAATTGATT TTTCTTGATT TCAAAACGAG CCCAGCGTTC ATCGTCCACA AGGCCAATCT	9060	
CGCGTCCCAT CTCATCAAG CGCATATCAG CATTGTGATG ACGAAGAATG AGACGGTATT	9120	
CAGCACGACT GGTCAAGAGA CGGTAGGGTT CAATGGTTC CTTGGTCACC AAGTCGTGGA	9180	
TCATCACCCC GATATAACCA TCACTGGGCT TCAAAATCAA TTCAGGCTTG CCTTGATTTT	9240	
TCAGAGCGCG ATTGATAACC GCGATAATCC CTTCGCCCTG TGCTCTTCG TAACTGATG	9300	
TTCCATTGTT CTGACCAGCA GTGAAGAGAC CTGAGATTTT CTTGGTTTCC AAAGTCGCAC	9360	
GCAACTGATG AGGCAAGACC ATATCATACT CAATAGACAA ACCTGTCCGC ATCATCTCTG	9420	
CATTTTCCAA ACCTTTGATG GAATGCACCA AGTCAAGCTG GACATCCTCA GGCAGACTGG	9480	
TTGAAAGTCC TTGCACATAG ACTTCCTCAG TATTGCGCCC TTCTGGCTCA AGGAAGAGTT	9540	
GGTGACGTTT CTGTCCGCA AAGCGCACAA TCTGTCTCTT AATCGACGGA CAGTAACGAG	9600	
GCCCCACTCC CTTCACCACA CCGTAAACA TAGGCGCACG GTGGAGGTTG TTTTGATATA	9660	
TCTCATGACT GGTACCATTG GTATAGGTCA ACCAGCATGG TACTTGGTCC TTGACATAAT	9720	

1219

CCTCATCAGC TGAAGTGTAT GAGAAATGAT TAGGCATCTC GTCTCCTGGC TGAATTTCTG	9780
TCACATCGTA ATTGATAGAA GAAGCCTTGA CACGTGGAGG GGTTCCTGTC TTGAAACGAC	9840
CGATTTCCGAG ACCCAGTTCC TTGAGATTGT CAGCTAGGTT AATAGAAGCC AAGCTGTGGT	9900
TAGGACCTGA TGAGTACTTG AGGTCTCCGA TGATAATTTC CCCACGAGA GCAGTCCCCTG	9960
TCTTCACAAAT AACAGCCTTA GCAGCATATT CTGTGATGGGT GGTCTTACGC ACACCGACAA	10020
CCTTGCCATC TTCCACAAA ATCTCATCAA TCATGGTTTG ACGAAGGTC AGATTTTCTT	10080
GGTTTCAAC CGTCTTGCGC ATCTCCTTAG AGTAAAGTTC CTTGTCAGCC TCGCAGCAA	10140
GGCAACGAC AGCTGGCCCC TTCCCTGTGT TTAGCATCTT CATCTGGATG TAAATCTTGT	10200
CAATGGTTTT GGCCATCTCG CCACGAGGG CATCGACTTC ACGCAGACA ATCCCTTGG	10260
CAGAACACC GATAGAGGA TTACAAAGCA TGAAGCCAG CATTTCAATA TTGATGTTG	10320
CAAGCAGGAC CTTACAGCC ATACGGTAG CGGCCAAGGA AGCCTCAACC CCAGCGTGC	10380
CCGACCAAT TACAATAATA TCTATTTCTT CAGTAAATG ATAAGTCATG TTTCTCTCT	10440
ATTCTCAAG ATGAATGTGT CTTAGTTGGC CTTCCTCAAT TGGTAGGGT GTTTTTAAA	10500
AGACTGGAAC TAGCTGGATA TTCTGAGCT TATCCAATC AATCCAATCA CAGGGCTGCC	10560
TTTTCTCATC TTCTGCTGATG GTCAACGGGG CATCTTCAAG CAATCCACC AGATAATGAA	10620
ACTCGATATT GTGATAGAA ACGCCGTCCA CTTCAAAACG ATTTTCAACC ACAAAGCTA	10680
GCTGCCAGC TTGAGCTTTO ACACCCAGTT CTTCCTTCAC TTCACGACT ACCGCTCTT	10740
CCGTGCTTTC ATTGACTTGA ATCGCACCTC CAATAGTGA ATACTTGCCC TTGTCTTTGG	10800
TAACTAGAAG CTTGTGATTT TCGAATCA AGGCTGTAG CCGAACACCA AAAACCTAT	10860
TGTCTACTTT TGTCCGAAAG TCTTGTGTAG TCATCTTGT CTTTCCCTT AAACGACAA	10920
AAAACAGTCA AAATACAAA GAAATGCAGG ACAAAGGAG CTGCAACATC CAGG	10974

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

CCCCTTATGA TTATGATAG CGCTTTCAAA TTTTAAACT CCTATCCCAT CCTTTATCT	60
ATATATAAG TGAAATATA ATAACTGTCA AGTAACTGAA GTGAATTTTA TAAAAAATT	120

1220

ACAAGCCAAA TTGTAAAGT TTACACTAAG CCGCTAGgCA ATCGTCTATC AGAATATCCG	180
TTTATTTTGTC AATAATCCGA GAAATCTTG CAACGCTTAG AAGTCTATAA AAACATATCAA	240
CATTATATG ACTTGCGAAT AGCAATCCTG CTPAAACCTTT CCACACTCTA TCTATACAAT	300
CAAGATAAAA ACATGTGTAA GCAATCTGC TACACTTTAC TGGAGGACGC CAAGAATAAG	360
AAAGGCTACG ATAGGCTTGC TATCTGCTAT GTCCGTATTG GGATTGTGAC AGACGATTCT	420
AAACTTATCC AAAAAGGGTT CTCCCTCTG GAGCTGACGC AGGAACTTC TATGCTGTCT	480
CATCTCAAAA AAGAAGTAGA GACCCATTAT CAACCAAAGA AATTATAAAA AAAGTCGAGG	540
GAGCTCCTCG ACCTTTTCAT AGAATCGCCG AACGATTTAA CGAGAAAGTA TGACTTTTAC	600
GTTTATCCCA ACTCAATTAT GACATTTTTT TCAAAAGTCA ATATATCTCA CTTTTCACAC	660
GACAAGAAAG AGGCTGATAA TCTACCAACC TCTTATCTG AACCCATCAC TCCATCACTT	720
TTTAGCTTCA TTGCTTTCT TAGCGACTGC AATCTGGTAT TCGACTTGGT CATTCGCCCT	780
ACCGGTACAA CCATGACGAA TTGTAGTCGC TCTTATCTGA TCGCTATT TCAACCAATT	840
TTTAGAAATC AGAGGGCGGC TCAAGGCAGA TACCAAGAGA TACTTTTGT CATAATAGGC	900
ATGTGACTGA TGAGCCACTA GCACATAATC TGTAGCAAA TCGTCTCTAA CATCAATGAC	960
ATAAGATTCT ACTGCCAAA CCTTAAG	987

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2651 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CTGGGTCTTG TTCATAGTAG GTGTGCTCT TTTTTCGAG TGAGCCCAT AGCTTTGAGC	60
GCATAGTGA TGCTAGTGG ATGACAGCCA AAGTCAGAAT CTATTCAGT CAAATAAGCA	120
TCTGGATTGT CAGTAAGATA GTTTTTAAGT CTATCTCTAT CAACTTTTCT TGGTTTTGTT	180
CTTTTACTT GGTGGTTTAC CTCCTCTGTT TTCTCTTTTA GCTTTAACCA GCCATAAATG	240
GTATTACGTG AGATTGGGAA AACGTGTGAT GCTTCGTGA TACTACCTAT TCGCTCACAA	300
TAAGAGAGAA CTTTTTTACG AAAATCTATT GAATATGCCA TAAGAAGATT ATACCACATT	360
GTCTACTATT TTTGGTTTAT TTTACTATAT TTTATAAGTT ATAGTGTAGC ATTCCAACCT	420
CAAAGCACTA TAAAGTAAAT TGAACAAGA ACAATACAAA CAATCTCGT AAACGGATTG	480
CAACCACAAA AAAGCAGCA TTCAACAAGA TACTTACCTA TCATGGGAGG AACAAACGGT	540

1221

CCTCTTTTT ATTACTAAAA TTCAAAGAAT	TCCAATGCTT	TTTTCAAGAG	CAAATCCGTA	600
TACTCTGGAT CTCTCTGGC TACTTCTATT	TCCCGCTGAA	CTTTTCCAA	ATCATCTGTA	660
ATCACTCCAT CTACTCCTAA GTGAAGAGAT	TTGCTGATAG	CTTCTGAATC	ATTGACAGTC	720
CAGACATAAA GTTCTCTGATC CGTGTCCAT	AGTTTGCCTA	CAAAATATTC	ATCCAAGGTT	780
GAGTACTCCA TAGTATATCC TGTGCTCTT	GTTTTAGGAA	AGACAGAATT	GTAGGCCATG	840
ATGAAATAAA CTGGTAGTTC GGCATCATAC	TGCTTACTT	TTTCGACAAC	ATGCTAGTCT	900
AAAGACTGGA TTTGATGTCC ATAAATCTTG	AGCTTTGCAG	CATAACGGCC	TAAAAAGCOG	960
TTGATCATGT CTGGACTATC TTTTTTACTG	GTTTTAAFTT	CAATTAGTAA	TTTTTGACCA	1020
AGTTCTGTGG CTGACTGAG ATAATCTTCA	AAGCTTGAAA	TTTTAGTCTG	GTAGCCATTT	1080
TCAAAAATAT CAATCCCTTT AAGCTCCTCC	AAGTTTAAGT	CTTGAGGACT	TTTATTGATA	1140
CCTGCTAGAT TTTTCAAGTT AGCATCATGC	ATCATGACAA	ACTGCCCATC	TTTTGTTTCC	1200
TGCAGTCCG TCTCCACCAA GTCTGTTTG	AGTTGTGCTG	TAGTTTCCAA	GGACTCTACT	1260
GTATTTTGAA TCCCATTTGC ATTGGAAACC	CCTCGGTGAG	AAATAAGTTG	AGGTAGATGA	1320
ACCATGGGAG CTTCCAGATA AATATAACCT	TCTAAGCCAA	AGAAAAGACT	GGCACAAGTC	1380
ATGACACCCC ATCGCACGAT GTGATCTTTT	TCTCTCTAG	GAAGCATATC	CAGCTCCTTT	1440
CCTGTCAAAA ATGAAACAAA TTTAACCAAA	AAATAAGTCA	GAGCCATATA	ATAGAGATTT	1500
TTAATCACGA CAAAATTCAA AATACCAAGA	ATCAGAGACT	CTCTCTGAGT	GATATCATCT	1560
ACCAAAGTTT GAGCCATATA TAAAGGAATC	AAAGGAAGAT	AAATAATAAA	ATGTGCTTTG	1620
AGCAAGATGT AAAATAAATT CCAAGCATAA	AAAGTAACTC	TCTTCTTGCT	TTTCTCCAAAG	1680
CTAAACATCA CTGCTTCTCG AACAGTCAGC	TGATCATATA	CAATCTTCGG	AAGGCCAAAC	1740
ATCAATCTGA CAGAGACATA GAGAAAGATA	AGAGATAGAA	GTAGGATGCT	CAGGCCACCAC	1800
ATCCAATATC TATCTTCTAA ATAAGCTTGG	ATAAAGCTCTG	GAATGACGAT	TTTATTAGAA	1860
TAATAAATCT TCAGCATTTT CCGTATAAAA	GGAAACAGCA	TAGCTATATA	GAAAAAGATA	1920
AACAAGGCTT TAGCGCAAGT TAGCTTTTTT	ATAAATCCAA	AACCTTTCATG	GAAAAACCTTG	1980
CGGATATACT CAATTAGCCT TCGCTTTTCA	TTATAGAGGA	GATGACGAGC	ACCAATAAAG	2040
AGGATCTCTA TTTGAAAAATA AGCAACAGGA	AGGTTAATTA	CAATCAAGGC	TAAAAAAGCT	2100
AGACTAATCA ATGGAGAATG AGTAAGGATG	GCTAAGACAT	TGTTATAGGA	AATAAAAAGA	2160
TAACCTGTCT GATCTAATAA GAAGCTAGCC	AACCATGAAT	TGAATGGTAC	CCACAAATAC	2220
TCCACTATCA TAAAAATCAA GAAAAATAGA	AAGAGGATTT	TATCAAGATC	GAGTAAATTC	2280

1222

TGTTTAAGAC CCAATTTTT AGGTTTTCA GGTTTCATAG GCACCTCTAG TCAAAATAAT	2340
GAGACAAGTC CAAGCCACCA AAGGATTGT TGATAAGCT ACTTTCCTGC TCTAACAAAT	2400
CCCTAGCTTG ATCCGACTCT AAGAAGGATT CGTAAACACG CGCCGTCAATC CGAGCATCCT	2460
CTAACTATCT ATGAGACTGA CCTTGAATC CAAGAAATGA GGCAACAGTT TGCATTTTGA	2520
GATTGGCAAT ACCATGTAAA TCTGAATCC GACGTTCAAA AGCTTCATCA TACAAATCCA	2580
CCTTGTAAGT TTGGCTATAG TCTAAACCAT GCTCTGCTAA AATAGGTAAA TCACCTTTAG	2640
CAGCATTTGA G	2651

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5638 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CGTTATAATA AACTTGTGAA AAAATTAAACA AAGGATATCG TTCCCTTGAAA GCTATGGAGG	60
AAAAATATGGC TGAATAAAAA ACTGTGACAC CAGAGGAAAA GAAACTCGTT GCTGAAAAAC	120
ACGTAGATGA GTTGGTTCAA AAAGCTCTAG TTGCCCTTGA AGAAATGCGT AAATTGGATC	180
AAGAACAAGT TGACTACATC GTTGCCAAAG CATCAGTAGC AGCTTGGAT GCCCACGGAG	240
AAATGGCTTT ACATGCCCTT GAAGAAACAG GACGTGGTGT ATTTGAAGAC AAAGCAACTA	300
AGAACTGTGT TGCTGTGAAA CACGTAGTAA ACAACATGGC CCACACTAAG ACAGTTGGCG	360
TTATCGAAGA AGACGATGA ACAGGATTGA CTCTTATTGC TGAACCAAGT GGTGTGTGTT	420
GTGGTATTAC TCCAACAACA AACCCAACT CAACAGCAAT CTTCAAATCA TTGATTTTAT	480
TGAAGACACG TAAACCAATC GTCTTTGGCT TCCATCCATC AGCACAGAA TCATCTGCTC	540
ATGCAGCTCG TATCGTCCGC GATGCAGCTA TCGCAGCTGG TGTCTCTGAA AACTGTGTGC	600
AATGGATTAC TCAACCATCT ATGGAAGCAA CAAGTGCCTT TATGAACACC GAAGGTGTTG	660
CGACAATCTT TGCACACGGT GGTAAATGCA TGGTTAAGGC GGCTTATTCA TGTGGTAAAC	720
CAGCTCTGTT GGTAGGTGCC GGAACCTTC CAGCTTATGT TGAAAAATCA GCAACCATTC	780
GTCAAGCAGC ACACGATATC GTCATGCTTA AATCATTTGA TAAAGGTATG GTCTGTGCAT	840
CTGAACAAGC AGTTATCATT GATAAAGAAA TTTACAGTGA ATTTGTAGCA GAGTTCAAAT	900
CTTACCACAC TTACTTTGTA AACAAAAAG AAAAGCTCT TCTTGAAGAG TTCTGCTTCG	960
GCCTCAAAGC AAACAGCAA AACTGTGCTG GTGCAAAATT GAACGCTGAC ATCGTTGTGA	1020

1223

AACCAGCAAC TTGGATTGCA GAACAAGCAG GATTTACAGT TCCAGAAGGA ACAACATTC	1080
TTGCTGCAGA ATGTAAAGAA GTTGCCGAAA ATGAGCCATT GACTCGTGAA AAATTGTCAC	1140
CAGTTATTGC AGTTTTGAAA TCTGAAAGCC GTGAAGATGG TATTACTAAG GCTCGTCAAA	1200
TGGTTGAATT TAACGGCTTT GGCACTCAG CAGCTATCCA CACAGTGAC GAAGATTGA	1260
CTAAGAATT TGGTAAAGCT GTTAAAGCTA TTGGTGTAT CTGTAACTCA CCTTCTACTT	1320
TTGGTGGTAT CGGGGAGCTT TACAATGCTT TCTTGCCATC ATTGACACTT GGATGTGGTT	1380
CTTACGGAGC CAECTCAGTT GGGGATAACG TTAGTGCCAT TAACTCTTG AATATCAAAA	1440
AAGTCGGAAG ACGGAGAAAT AACATGCAAT GGATGAACT TCCTTCAAAA ACATACTTTG	1500
AACGTGATT C AATTCAATAC CTTCAAAAAT GTCGTGACGT TGAACGTGTC ATGATCGTTA	1560
CTGACCATGC CATGGTAGAG CTTGGTTTCC TTGATCGTAT CATCGAACAA CTGACCTTC	1620
GTCGCAATAA GGTGTTTTC CAAATCTTG CGGATGAGA ACCGGATCCA GATATCACAA	1680
CTGTAAACCG TGGTACTGAG ATTATGCGTG CCTTCAAACC AGATACCATC ATCGCACTCG	1740
GTGGTGGGTC TCCAATGGAT GCTGCCAAG TAATGTGGCT CTCTACGAG CAACGAGAAG	1800
TGGACTTCGG TGACCTGTGC CAJAAATTCA TGGATATCCG TAAACGTGCC TTCAAGTTCC	1860
CATTGCTTGG TAAGAAGACT AAATTCATCG CGATTCCAAC TACATCTGGT ACAGGATCTG	1920
AAGTAACACC ATTTGCCGTT ATCTCTGATA AAGCAACAA CCGTAAATAC CCAATCGCTG	1980
ACTACTCATT GACACCAACT GTGGCAATCG TAGATCCTGC TTTGGTATTG ACAGTCCAG	2040
GATTTGTGTC TGCTGATACT GGTATGACG TATTGACTCA CGCGACAGAA GCATACGTAT	2100
CACAAATGCG TAGTGACTAC ACTGATGGTT TAGCACTTCA AGCCATTAAA TTGGTCTTTG	2160
AAAAATCTGA AAGCTCAGTT AAGAAATGAC ACTTCCACTC ACOTGAGAAA ATGCATAACG	2220
CTTCAACAA CTCTGGTATG GCCTTTGCCA ATGCCCTCCT AGGTATTCTT CACTCAATGG	2280
CCCATAAGAT TGGTGCACAA TTCCACACAA TCCACGGTCG TACAAATGCT ATCTTGCTTC	2340
CATACGTTAT CCGTTACAAC GGTACACGTC CAGCTAAGAC AGCAACATGG CCTAAGTACA	2400
ACTACTACCG TGCAAGTAA AAATACCAAG ATATGACAGC CATGCTTGA CTTCCAGCTT	2460
CTACTCCAGA AGAAGGGGTT GAATCTTACG CAAAAGCTGT CTACGAATC GGTGAACGTA	2520
TTGGGATCCA AATGAATTTT AGAGACCAAG GAATTGACGA AAAGAATGG AAGAACAATT	2580
CTCGTAATTT AGCCTTCTCG GCTTATGAAG ACCAATGTTT ACCAGCTAAC CCACGCTCTC	2640
CAATGGTGA CCAATGCAA GAAATCATCG AAGATGCAAT CTATGGCTAC AAAGAAAGAC	2700
CAGGACCGCG TAAATAATTG TTTATCAGTC TAGAAGCAAG ACAAAAATC AATTGAGGG	2760

1224

AAAGATCCAG TAAFTTTTCT ATGATAAAAG GCATCCTATC AAGGTTTTTG AACACCTGAT	2820
AGGATGCCCT TTTATGATAT TGAGGCCCTT TGCCCTTTT TGAJJAACTA GANTAGAAAC	2880
AAAATATATA ATAGATTGAA ACTAGAATAG TACATATCTG CTCTAAAAAC ATTGTTAGAA	2940
TTGATTTTGA CTGTCTGTAT CGATTGTGCC TGTTCTTATT TCATTTTGAT ATATAAAAAA	3000
TATAGATAG TAGACTGAAT CTAAAAAGT ACGAAACAAT TGCTAAAAACA TTTATAGAAA	3060
TTAATTTTAC TTTTCTGATA GAGTTGTTC CATCTTATT CAATTCACTA TAGTTTAAAT	3120
TAAGAGTAGT ATTACTAAG GCCCAATTAA AATCAAAGAG CAAACTAGAA AACGAGTCCC	3180
ATTGAGCTCA AAACACTGAT TTGAGATTGC AGATAAGACT AGCCCCCTCA TTAACAGATT	3240
TACGATAAAA CGATGACAAG GTGTGTGTCT TTTTGATTTC TAAAGAGTAT AATGATAGAT	3300
CTCTATAAAA TAAGTCCGAA GGAAATGAGC TTTTATAGTC CTTCGTGTT AAAATACTAT	3360
CTCAGATATT CTTATATCGA CAAGAAGTTT TTGAGTCATT CCTTCATCAT ACATATTAAA	3420
TAAATAGTGG CTCATTCAAT TTTTCACTAG AATAAATAGC TAGTATAGTA AACTGAATAA	3480
AGATATATAAC AATAAAATTG GAGCTTAACA TCCATTTCCT GCAATTTTTT AGAAACTACA	3540
GTGGACTATT CTAGATTCAA CATATTATAA AAACAGAGT AAAAGAAAAG GATTGGATCT	3600
TGTGTAATGC AGGATCCAA CTCTTCAATC ATTTTGTCCTA ACTTTTGGAG GTTCTACAA	3660
TGTAGTCGTC ATTAATAAAG ACAGATGGGA ATGACAGTGT TCCTATTAT TTTGATAGAG	3720
ATCGATGAAT TCTTTAGATA GCAACTGAAT AATCTCTGTT GAAGCAATT GCTCTCTGC	3780
ATCGATAAAT AGCAAGGAGA ATCCTATTTT TTCTCCAGTA GCTTCTTTTT GTATGAGATT	3840
AGAGTGAATC TTGTGCGCTT CTACTAAGGA GTCTCCGCT TCPTCAACT TAAFTTTGCG	3900
TTCTTTTAAA TTTCCTGCCT TAGCTAGTTG GATGCGCTCA ATAAAGGATG ATTGGCTGC	3960
TCCACTATG GCAATGAGCT GAAAACAGAT ATATTCCATT TCTTCTGTCA TCTTATTCT	4020
CCTATCCATG CAAGTGCCTG TTCCAGAACT TTTGCTCCAT TCATCATCC GTAAATCCCGC	4080
ATATCAATGG TATCTACAGG GATATTCTCT GCAATTCTT TCACAGCAG TAACTCATAA	4140
CGAATTGTG GCCCAATTAG AATGACATCT GCTTCATGGA TATTTCTTTT AGCTTCTGTC	4200
ATTGATTTTG CTGGATAGA GATTTCATCT CCAAGTTCAG TCAGACTTTG TTGCATTTTT	4260
TTAACAAAGCA TACTTGTGCA CATTCGCCGA TTACATACTA ATAAATTTG TTTCAATAAC	4320
TTAACTTCC ATTTCTGTGT CAACAACATT GTCAATAACT TTGATAAATG GAATGTATAG	4380
AAGAACTCCA AGTGCAAGA TGATGAATTG AACTAGAACT GCTCTCACTG CCCCCTGCTG	4440
TGCTAACCAT GCAATTAAGA ATACTGCTGT AGTCCAAGGA ACTGTGTATA ATGACAGACT	4500
CATGAATCT GTAACTGTGT CTAAGTAGCT GATTAAATA CCAAGGACTG GAACGTGAT	4560

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AAATGGAATA GCTAATGAAA TGTTATAAAC GATTGGGTAA CCGAATAATA CTGGTTCAAT	4620
GATATTGAAG ATACCAGGTC CAAAAGATAA TTTAGCCACG TTTTAGAGAG CAGCATTGCG	4680
ACTCACTAAG AATGTTGCTA TTAATAAACA TAATGTAGAT CCACTACCA CCAATAAAGC	4740
GAATGCTTGT ATTTGTGATA GGTTGATGAT GTGTGGAAAT GCTTGTCCAT TAATTGCTGC	4800
AGTGATGTTT TCAGTAATGT TAATTAAATAG TAATGGTTCT AGGATGGCAG TGTAAATAAC	4860
TGCTTGGTGA ATACCAATAA GCCATAACAT ACTTCCATAA GAGTAATAAA TAATGACCCC	4920
GATTAAAGCT GTACCAATAT GACGAATTGG TTTTGTAATA AAGATTGTAA TGATTGAGAT	4980
TAAGTTCAAT CCAGTTATAT TGAATAATAA TGCTGAAACA ACCCCAAATA AGGAGATGAC	5040
GCTCATGACT GGAAGTAATA CGCTAAATGA TCTACTAACA GCTGGTGGAA TATTTTCACC	5100
AAGGTTCAAT TGTAAAGCTT TAACGTTTGA TAATTCAATG AATAATTCTG TTGCAATAAT	5160
CGTACGATAA CCCCGGGGAA CATTCGCGCT GTACCTGTGT TGTGAATGA AAGAACACCT	5220
GAAATGTTTA CCGCATCTTT TGCTCCGTCA GGAACACAG AAACGTGTAT TTGCATCATC	5280
ACAAATTAAG AAACATAATGA TAGCATTGAT GCTGCTAACG GGTTTTCGAA ATCTCTGTTT	5340
TTAGCTAAGA AATAACCAAC CATTCACGCA ATAAATCATC CTGAATAATC TAAAGTACCG	5400
TTTGCAATFG TTAATCCOCA ATATTGGAAT CTGTGTAATG TATCCCTTGG GAAATCCAC	5460
TTAAATACCG TGTGTTCAA AAGAACGATT AAACCTGCCA AAATATATAA TGGCATTAAT	5520
GTTACGAATG CATCTCTTAG GGTTTTAAAA TGAATTTGGT TCCCTAGTTT ACCAGCAAAG	5580
GATGGCAAAA AAATTTTTTT GGGGGGGGGG GTTATTAAAC CCCCCTTTTT AAAAAAAA	5638

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CCGGAAGCTG TTGCCCTTGG AACTCCAAT GAAGAAACAG CCTTGTCTT GAACATTTTT	50
GCTGTGGAAG CACCAAGTGT TATCACTTCT GCCAAGCAG AGGGGGCAGA GCAAGTTATC	120
TTGACTGACC ACAATGAAT CCAACAATCT GTATCAGATA TCGCTGAAGT AGAAGTTTAC	180
GCTGTTGTAG ACCACCACCG TGTGGCTAAC TTTGAAATCT CAAGCCACAT TTAATGCGT	240
TTGGAGCCAG TTGGATCAG GTCTTCAATC GTTACCGTA TGTTCAAAGA ACAATGCTGA	300

1226	
GCTGTGCCCTA AAGAGATTGC AGOTTTGATG CTTTCAGGTT TGAITTCAGA TACCCTTCCT	360
TTGAAATCAC CAACAACACA CCCAACAGAT AAAATCA'TTG CTCTTGAATT GGCTGAATTTG	420
GCTGTGTGA ACTTGGGAAGA ATATGOTTTG GCAATCTTGA AAGCTGGTAC CAAC'TTGGCT	480
AGCAAACTCG CTGAAGAATT GATTTGATATC GATGCTAAGA CTTT'TGAAC'T CAACOGAAAT	540
AATGTCCGTG TTGCCCAAGT GAACACAGTT GACATCGCTG AAGTT'TTGA ACGCCAAGCA	600
GAAATTGAAG CTGCAATGCA AGCTGCCAAC GAATCAAACG GCTACTCTGA CTTTGTCTTG	660
ATGATTACAG ATATCGTCAA CTCAAACTCA GAAATCTTGG CTCTTGTGTC CAATATGGAC	720
AAGGTGGAAG CGGCTTTCAA CTTCAAAC'TT GAAACAATC ATGCC'TTCTT TGTGGTGGC	780
GTTTCACGTA AGAAACAAGT GGTACCTCAA TTGACTGAAA GCTTTAATGC GTAAAGATTTT	840
GGGTGTCAGC TCAAAATCGG AAAGTCTAGT TTGCC'TTATA TCGCAAGGAG TTTTCGGCTCC	900
TTTTTTCTAG GAGTGAAGTA TGT'TAGAAAA TGCGCATTTG ATTTT'TGTGA GAGATGGGTC	960
AGACGTGGGA CAGGCCATCC AGACTTCCAC AGGTAACTAT AGCCATGTTG CCATTTATTTT	1020
GGATGGGATG ATTTATCATG CTAGTGGACA GGTGTGTGTT GTCTGTCAAG AACGGGCAGA	1080
CTTCTTTGAG TCCAACTCAT TATACGACCT CTATGTTTAC CCAGAAATGG ATATCCAGTC	1140
GOTGAAGGAA AGAGCTTGCA AACATCTTGG AGCACCTTAC AATGCTTCTT TCTATPCAGA	1200
TGCAGCTGGT TTTTACTGCT CCCAGTATAT AGCAGAAATC CTACCTATTT TTGAAACTAT	1260
TCCATATGAA TTTGGAGWTG GGGAGCAGGA GATTAATGAT TTTTGGAGGG AGTATTACAT	1320
AGAACTAGGT CTGCC'TGTC CTCTGAACCA AGCTGGTACC AATCCTAGTC AGTTGSCAGC	1380
ATCGCCTCTG TTACAAATGA AAGAAAGGAA TCTTCAATGAT TCAGATTTTT AATCCATCTC	1440
GTTTGACGAG ACAGCCATTT TTGGAGAATT GATCCGCTAT CTGGATCAGT ATGAGGATGT	1500
GATTTCTACGG GAAATTAAGG CTCAA'TTCC AGATGTGTGA GTTGATAAAC TCATGGGAAGA	1560
GTATATATAAG GCAGGCTTGA TTTCTAGTGA AAATAAGGCG TATTACCTCA ATTTTCTTAC	1620
GCTTGAATCA CTTGATAGTC TTGAAC'TGGA TCAAGAGATT TTTGTCAAG AAGCTAGTCC	1680
GGTCTATCAA GCCTTGT'TGG AGCAGAGTTT TGAGACGGAA TTGCGCAATC AAATCAATGC	1740
AGCTATTTTA GTTGAAAGA CGGACTTTGC GCGCATTAAG ATGACCTGTG CCAA'TTATTT	1800
TTACAAAGGT AAACAGCAGT ATCCTTTGAC AGAAAAACAG CAGGAGCTCT ATGACATTTT	1860
AGGAGATGTT AATCCTGAGT ATGCCCTCAA GTATATGACG GCTTTT'TGT TGAATTTTCT	1920
CAAAAAAGAC CAGCTTATGC AGAAATGCCG TGAATATCTT GTGGACAGTT AGGTTGTCTT	1980
AGGCTATATT GTGCAAAATG AAGATGGAAA GTATGAGTTG GCTATGCATT TTGATAAGGA	2040
GAGGTAACT TTCTACTTAG CGTGATTCTT TGT'TCTGAG TACATTGTTT GACTTTCTCT	2100

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AGTATTGGT ATAAACTATA TGTAACTGTT AACACATATC GGAATAAACT AAAGGAGACA	2160
ATCATATGTC ACITGAAAC AAATTGGAAC AAGCAACAGG CGCTGTCAA GAAGGTTTTC	2220
GTAAAGTTAC TGGAGACAGC AAGACAGAAC TTGAAGGAGC TGTTGAAAA ACAGTTGCTA	2280
AGGCAAAAGA CCTCTAGAA GACGCAAAAG GTGCTGTAGA AGGTGCGTT GAAGTTTGA	2340
AAACGTTTT TACTAAAGAA TAGGAAAAA TCAGGGTTT CATTTCCCT TGATTTTTTC	2400
TATTTCTATA AATAATTTTC TGCGACGGCT GTATCTCTTG GGTAGGATTC TTTCTGCCC	2460
TGGATGATTT GGTAACAATC GGCTCCCTTA CCGCAATTA TAATGTCATC TAATTCGTGA	2520
TTTGTGATAG CCATTCGCGC CTGTATGGCT TCTTGGGAT CCGCAATCTT TTCAACAGGA	2580
TGATTGATGT AGCTACTAAT TTCACTGCA ATGGCCATTG GGTCTTATA GTTAGGGTCA	2640
TCAGCAGTCA GAAAGACTTG AATCTCAGGG TGTGATTGA GGAGGAGGCC AAAGTCCTTA	2700
CGACGACTTT CTCCCTTGTG TCCGTGTGAT CCCAGAACCA GAGCAATCTT TCCGTTTGA	2760
TGAGTTTCAA CCACATTGAT GAGTTTTTTC AGACTATCCC CATTTGTGGC ATAGTCGATG	2820
AAGACCTTGG CTCCATTTT CTGAGTGAG ACTTCCATAC GACCAGGAAC GCGGTTTGA	2880
CGGATGCCCT TTTTGTGTC CTCAAGACTT GCTCCGAGC GGAGACAGC AAGTCCAGCA	2940
GCACTGCAT TTTCTTGGT GAAGTTGCCA ATGAGTTGAA TATCATATC TCCAGCGAGT	3000
TTACCGGTAG CTGAAAAGCT AAGGCTTTG GAATCTTGA TTTGGTTATC AAATTGGCTA	3060
CCATAGAAAT CATGCTCTTG ATCTTCAACC TGTCTTTCA AGACTGAGAA GTGGTCCATG	3120
TCACGTGTA TGATGACTGC TCGGCTCTT TCCATCAAGA GACGCTTGTG GTAGAAATAG	3180
TCTTCAAAGC TAGGCTGTTA AATCGGGCCG ATATGGTCTG GGCTGATAT TAGGAAAACT	3240
CCACATCAA AGGTAGAGC ATAGACAGCT TTGACCAGAT AGGCTTGACT GGAGACTTCC	3300
ATGATGAGGT GGGTACGGTC ATTTTGCACA GCTGATTCA TCATGTCAA GAGGTCAATA	3360
CTCTCAGGGG TTGTCAACGC TGACTTAAAG AAGTCTCGC CATCAAGAT TGTGTTCTAG	3420
GTGACAACA TAGCAGTCT ATGCCCTTGA GATAAGATGT TATAGCGGAA ATAGGCTGCT	3480
GTTGTCTTAC CCTTAGTACC AGTAAAGGCA AGGAGTTTGA GTTTTCTCTG TGGATTACCA	3540
TAGAACTCCA TGGCAATCAA ACTCATGGCT TTTCTTATAT GGTTCACAT GATGACAGGG	3600
ATACCGACTT CGTAGTCTT TTCACTACA TACCAAGCTA ATCTTGTGT TATAGCAGAA	3660
AGAAGGTATT CTTTTTAAA GGCAGCGCTT TTTGCAAAA AAAGAGTGT TTTCTTACT	3720
TTTCGGCTGT CGTAGTGTAT GCTATCAAAA ATAACTTTTC TGTAGTTGTA GTGGTAATGA	3780
CCTTGGTCAA TAATTTGGG AAAAAGGCCA TCTTTCTTAA AATATCTAA TACGGTTTCA	3840

1228

ATCTTAATCA TACTTTCTAT TGFAAACCGA AAGTCGTAAA TTTCACAGTA ACAAGGAAA	3900
GTTTATAATG GAAGATAAGG AGTTTTCCT AGTTATCAAA ATTGAATGAG GAATCTATGT	3960
CGCACGAAAA CAATCACCAG CAGGCCAGTA TGTTACGGGG GACTGCTTGG CTAACGGCTA	4020
GTAACCTTAT CAGTCGCCCTA CTCGGGGCTG TTACATATT CCCTTGGTAC ATCTGGATGG	4080
GGGCTTATGC AGCTAAGGCA AATGGTCTCT TTACCATGGG TTACAAATC TATGCTTGGT	4140
TCTTGTGGT TTCAACAGCG GGGATTCCAG TTGCGGTGGC CAAAGCAAGTT GCCAAGTATA	4200
ATACCATGCG AGAAGAAAGAG CATAGCTTTG CCTGATTGCG GAGCTTCTTA GGCTTTATGA	4260
CAGGACTAGG CCTGGTTTTT GCTTTAGTCT TGTATGTCTT TGCTCCTTGG CTAGCAGACT	4320
TGTCGTGGGT GGGCAAGAGC TTGATCCCAA TCATGCAAGG CTTGCTTGG GGAGTCTTGA	4380
TTTTCCCGTC TATGAGTGTT ATCCGAGGAT TTTTCCAAGG GATGAATAAC CTCAAACCTT	4440
ATGCCATGAG CCAAAATGCT GAGCAGGTCA TTCTGTTAT CTGGAGTCTC CTAGCAACCT	4500
TTATCATATG GAAGTCGGT TCAGGAGATT ATCTAGCAGC CGTTACCCAA TCAACCTTTG	4560
CTGCCTTTGT CGGTATGGTA GCCAGTTTGG CAGTCTTGAT TTATTTCCCT GCCCAAGAAG	4620
GTTCACTCAA AAGAATCTTT GAAACAGGAG ATAAGATTAA CAGTAAGCGT CTCTTGGTTG	4680
ATACCATTTA GGAAGCATT CCTTTTATCC TGACAGGGTC TGCCATCCAG CTCTTCCAGA	4740
TTTTG	4745

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CCTGATTGAC CTTATAATAA GGAACAAAAC ACAATGCAT ACCTTTTCAA CAAAAGAGTT	60
GCTGCTTGAT TAAAACCATC ACACCAGTTA TACCATTTTG CTTTCATACC ATCTTGAGCT	120
AGGATACGAT CTTCTAAATC AAAACAGAG TAAATCTTTC TTTTCTCGCA AGCTTGGCA	180
TAGAGATGAT ATAGTTCATC ACCACCATCT CTATCCCAC CTAGCAGAAAT CGTATCCCAG	240
CTTGCCAATA AAGCCTGATA AGCCCTGTGA TGCCCATCTG TAATCAGCAA ACAATCTCCA	300
AAGGCAAGAA TACTGATTGG ATCGACTTGG ATTGTTTCTG CCGACTGGTA AAGCATCTGA	360
ATATCTTGCA ACTTCTTTTC TGATAAATAT AGTTGAGTCA GATGAAGATC TGCTATAATG	420
ACTTTCATTT CTCTCTCTCT AAGGGAATTC GATACTCACT TCTGTTCGC TTTAATTCGC	480

1229

CATTGGAAGC GGAGCTTGTC ATAAAAGGGA AACTCGATAA ACAGGACTCT CAAGCCCACA 540
 CAGAGACTGG CAAGGACGTC TGATGGGTAA TGAATCCCA GATAGACTCT TGATACCAGC 600
 ACACCTGACTA GGTAGAGGCC AAGGACGATT TGTACGATTT TTCTCCAGAC CTGATCTTTA 660
 ATCCGCTGAC TAAGATAAAC AATCAAAGTC CCTACCATCA GCGTTACAGC TAGAGAATCC 720
 CCACTTGGGA AGGAAATACC CTCTCCTCC ACCAGATGTA AAATAGCTGG TCGTGGGCGC 780
 TGTGTAGATAT TTTTAAAGGT CACGATTAAA AGACCTGCCA AAGCCAGATT TCCCGACATG 840
 AAGAACTTTT CTNTCTTCCA TCGCTTACGA TAAAGACAA AAGCTGTAAAT GACAACCCAA 900
 GTGATAATCA CTGGGATATC AATCAGACGT GTGAGGGCTC GAAAAAGAA AGTCAATAAA 960
 TCTGGTAAAT CTCTCGAAT GGCACTCTGA ATCGATTGGT CAAAATTGAC CAACATTTC 1020
 GGGTAAJAAT TGACCATGTA GCCAAGAATA ACGAAAAGTA AAAGGGCAAA ACTGCCCTTC 1080
 ATPAAAAATG TTGCTTATC TCTCATAATG TTTTAAAGTT GGTTCACGA GAACATACAA 1140
 CAACGAGAT GAAACGGAAA AGATAACACC TTCAATCAG TTAAGAGTA ATACCATGGT 1200
 CATTAGTAG TTGGAAAGTC CCAAAATTTT TCCAATATCA AAGTTAGCAA ACTTAGCGTA 1260
 CAAAGAACCA GCATAAACAT AGTTGAGAAC CAACATGGCC AAGGTTAAAC CAATAGTTCC 1320
 AGCTAGAGAG CCTAGTAGGA AACGAAAGGT TGTCCGTTC TTTTCCAAA TCAAAGCAAA 1380
 TACGATGACA AAAACTCCCA AAGCTACGAT ATTCATCGGC AAACCAATGT AAGTATTAC 1440
 TCCTTGGCTG TTAAAGACA ATTTCAAGAG TGAGCGAAGC AAGAGCACTC CTAGAGmC 1500
 AGGCAATCC ATGACCACCA GACCCACAAG GACTGGCAG ATACTAAAT CGATCTTGAG 1560
 GAAAGATGCC GCTGTAAAA GCGAAAGTC AAGTACATC AGCACAATG AGATGGCTGA 1620
 TAGAATTGCA ATGCTGAAA GTCGACGTGT GTTTGTGATA ACAGGTTCTT CCAATTTCT 1680
 ATAAATCAG AAGAAGTTGG AAGGATTCC TCTATCTATT CTCACTTTTT ATATCCCAAA 1740
 AGTTCCCTCT TACTCTATTA AAGAAAAACA AAGCAAGTGG TTCAATCCG GCTATAAATC 1800
 TATCAAAACA GACAAGGCTA TTCTTTGCTC TTCTCCATC CAGACTATAC TGTGGTGT 1860
 GGAATCTCAC CACATCAGT TGCCTCACG GACTTCTTTA 1900

(2) INFORMATION FOR SEQ ID NO: 220:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4692 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

1230
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

GGTTCCTCAG CAGGAGCTTC TCCTTTATCA GAATGACCAT CCATCTGCT CAOGATAGAT	60
GATATATGAT ATTTTATTACC ATGATAGTAA TTTGAAAAG CCTAACACC TCCTGAACCT	120
TCCTCCATATG TCCATVACTCC TCCATCTGGA TATTATACAG CAGCTGATGC AGCTCCCAAT	180
AATGTAAAC TTGAAAAG AGCTAGAGCA AGTAATCTAT GTTTTTCGT TTTTATTTTA	240
TTTTTCTTT CAAAAAAGC ACACCTTGAG CAACAATGCA ACAAATAAA TCCTCCTCTC	300
TCCTTTATTG AAACCGCTTT CTATGTGAT AAGAATACT TTTTATAT TTGTGTCAA	360
GGAAAAATC GAATTTTATA GATACTTAC TATATTACCT CTGTGAATA TATTATATAG	420
TAGTTTATAT TCAAAATAAT ATGCAACCAG TACTAACCA ATATATAATA GATGCCATTA	480
ACGAATTTTA TTCAAGTTTT TCCCATTCAT ACTATACAAG TAAAAGAGAT GGTGTAACT	540
AAAAAGCAAT TCAAACTATT GTAAAATCCC TAGCAAAAAG AGAGCCGAAA CTCTCTTTTT	600
TATCTCTTT TACTTTTTTT GACTGGCATG AGTGTGATGT CTCTAACCT AAAGTAAGCT	660
AGGATCAACA TGGCTATGCT TAGGAATATT TCTGTTGTA ATTGAAAAAT TTTCAAGAAA	720
GATAGAACCA ATAAAAACAA GAGTGCCACT AAAATACATA CCATAGCGAC GATATTGACA	780
GTCCCTTTAA TGCTTCTGG TGTCGCAAT ACATAGAGTA GGAGCAGTAA AATCCTTAGG	840
ACTAAATAGA CCATCTTTCT CTCTTCTAG CTCTTATCA GCTGATTTTT TCTTCTGGT	900
AGCTTCTCA CGCTCTGCT TGTAAAGGAT TTTTTCACG AAACGGTAG ACTCAGGCGT	960
TACTTCCATG TACTCATCGT CGTCAAGAA CTCAGAGAC TCTTCAAGTG TCAAGATAG	1020
AGCGCTCTTG ATACAGCTG TTTGGTCTT AGTAGCTGAA CGACGTTGG TCATTGTGTT	1080
TGCTTCTGT ATGTTAACTG TCAAGTCATT TTCAAGAGAG TTTTACCAG TGAATATTCC	1140
TTCAATAACC TCAGTACCTG GGTGACAAA GATCGTACCA CGTCTTCA TAGACATGAT	1200
TGAGTAAGTT GTAGCCTTAC CAGCATCGAT AGAAACAAG GCACACGGT GACGTCCACC	1260
AATTTCCCTT GGAATCAATG GCAAGTATTG GTGGAAGTA TGGTTCATGA TACCGTAACC	1320
ACGAGTCATT GATAAGAACT CAGTTGAGTA TCCAAACAA CCACGGCTG GAACAAGGAA	1380
GACCAAAAGA GTTTGACCAT TACCAGTTGA AATCATATCC AACATTTAC CTTTACGTTT	1440
AGAAAGGCTT TGGATAACAG ACCCTTGTA TTCTCTGGA GTGTCGATT GTACACGTTT	1500
AAATGGTTCA CATTAAATAC COTCGATTTC TTTTACGATA ACTCTCGAG GAGATACTTG	1560
AAGTTCATAG CCCTCACAG GCATTGTTTC GATAAGGATT GACAAATGCA ATTCTCCACG	1620
TCCTGAACAA GTCCATTAT CTGTGTAATC AGTTGGGTCA ACACGAAGGG AAACGCTCTG	1680
TTGCAATTCT GCCTGCAAG GTTCTTCCAC CTTACGAGAA GTTACCAATT TACCTTCTTT	1740

1231

ACCAGCAAAAT	GGTGAGTTGT	TGACCAAGAA	AGTCATTGTA	AGAGTTGGCT	CATCGATGTG	1800
TAGGATTGGA	AGAGCTTCTA	CTGCATCTGT	CGGAGTGATG	GTTCACCGA	CAAAGATGTC	1860
TTCCATFACCT	GAACCGCAA	TCAAGTCACC	CGCTTTGGCT	TCTTGGATTT	CACGACGTTT	1920
CAACCAAAAG	AAACCGAAGA	GTTTTGTAA	ACGGAGTTT	TTAGTTGTAC	CGTCAAGTTT	1980
AGAAAGGGA	ACTTTGTCCC	CAACCTTAA	TGTACCACGG	AAGACACGAC	CGATACCGAT	2040
ACGTCCAACG	AAGTCATTGT	AGTCCAAAAG	TGACACTTGG	AAGTCAAAAG	GCTCATCTGA	2100
GTATCTACT	GGAGCTGGGA	TATGGTCGAT	AATCGTGCA	AAGATTGGTG	CCATAGTCGC	2160
TTCTTTGGTCA	GCTGGATCAT	CTGACAAATGA	AGAACTTCG	TTGATCGCTG	AAGCATAAAC	2220
CACTGGGAAA	TCAAGCTGGT	CGTCATCTGC	ACCAAGCTCG	ATGAAAAGTT	CCAAGACTTC	2280
ATCCAATCTACT	TCTGCTGGAC	GAGCTGATGG	CTTATCGATT	TTGTTAACAA	CCACGATTGG	2340
GACCAAGGCT	TGTTCCAAGG	CTTTTTCCTAA	TACGAAACGA	GTTTTGCGCA	TGGTTCCTTC	2400
ATAGGCATCT	ACGACCAAGA	CAACACCGTC	AACCATTTTC	ATGATACGCT	CAACTTCTCC	2460
ACCAAAGTCC	CGGTGTCTCG	GTGTGTCCAT	AATGTTGATA	CGAGTTCGGT	TGTAAGCAAC	2520
GGCAGTATTT	TTAGCAAGGA	TGGTAATTC	ACGCTCTTTT	TGATATCGT	TTGAGTCCAT	2580
AGCACGCTCT	GCCAATTCAG	TCCGTGCATC	AAGCGTTTCT	GATTGTTTCA	ATAATTCGTC	2640
AACCAAGGTT	GTTTTACCGT	GGTCAACGTG	GGCGATAATC	GCAATGTAC	GGATATCTTC	2700
TCTTAATTTT	GTCAATGATT	CCTCTATAAT	ATTCAAAAAT	TATTTTCTAA	CTGAACGATT	2760
ATACCATAAT	TTCAAAATAA	TAACTAACT	CAAGCAAGTG	TAAATGTTTT	CACTCTGCTT	2820
TTCTTTTTCAC	GTCAAGCGCT	TTCAAGCGA	GCGACTTATG	ATAAGATAGG	CACAGTATGC	2880
GTTTAGATAA	TTTATTAGCT	CAAGAAAAAA	TCAGCCGAAA	GGCCATGAAG	CAAGCACTCC	2940
TCAGAGGGGA	AATTCTAGTC	GATGGTTGCC	CAGCCCGCTC	CCTAGCTCAA	AATATCGATA	3000
CAGGACTACA	AGAACTCTTT	TTTCAGGATC	GAATCAITCA	AGGCTATGAA	CACACCTATC	3060
TTATGCTTCA	TAAACCTGCT	GGTCCGTTA	CAGCCAACAA	AGACAAGGAA	CTTCGACCG	3120
TCATGGACCT	GCTTCCATCT	AACATCCAGT	CTGACAAGCT	CTATGCCGTT	GGCCGACTGG	3180
ACCGAGATAC	AACGGGACTC	CTCCTCTTGA	CGATAACCG	TCCCTTGGGC	TTTCAGCTCC	3240
TCCATCCCCA	ATATCATGTC	GATAAGACTT	ACCAAGTTGA	GGTTAATGGA	CTTCTAACAC	3300
CTGACCATAT	CCAAACCTTT	CAAAAAGGAA	TTGTCTTTTT	AGATGACACT	GTCTGTAAAC	3360
CCGCAAACT	AGAGATTCTA	TCTGCAAGTC	CTCCCTCAG	TCAAGCCCTCT	ATCACCATTT	3420
CAGAAAGGAA	ATTTTCATCA	ATCAAGAAAA	TGTTCTCTCT	GGTTGGTGT	AAGGTGACTA	3480

1232

GCCTCAAAAG AATCCAATTT GGGGACTTCA CATTTGAACC AGATTTAGCA GAAGTAACT	3540
ACCGCCCTTT GAACCAAAA GAGTTACAAA TCATTA AAAA CTATTTAGAG ATGAGTCGAT	3600
AAACAAAAA AAGCTTTAAA ACTAAAGCTT TTTTCTTTTA TTACCGAAA AATTAAGCGG	3660
ATTGCTACAA TCCAGTTAAC TACAGAAATC ACAATTCCTA AGATATTAAG AATCTTTTCT	3720
ATTTTATAGT CTAAATTGTA CTCTTTTGG TATGAAATAG CCAAGACCAA TCCTATGATA	3780
CCCAAAATCA GGCTTACAA TGGAAATAAC AAACCAAGAA TATTCGACAA GATACCCACA	3840
AAAAGTGGAT TTTTCTTCTT TCTTTTATG TTCTAAGAAC TCCTTAAAT TTATACAAAT	3900
TAATTTACT ATAAACAAT AGCTTCATCC TATCATTCGA CTAACTTGA AATAAGTTA	3960
GCTAGTCTTC ACTTTCCCTT TCCAAGAATC CAAGCCATAA GAAAGGATAT AANTCTCAGA	4020
AAAACCTTGT TTTTCAAGT AAAGAGCTGC ATTTGTAAT CTGTGCGCAC GTTGGTTTC	4080
GTAGAAGAG ACAGGTTTAT CTTTACGAAG GGCTGCAAGA CTAGTTTCA ACTGACTTGA	4140
AGGAATATTG CGTGACCAA GGATATGTTT TCTGTGGAAT TCTGCTGGGT CGCGCAATCA	4200
AATCAATTGA CCGTAGAA TCAAGGCTTC AAACCTCTCA TTGTCCACAA TTTTAGCCGC	4260
ACGGCGAATA CGAAGATAGT TAAAGCCCAT CCACGCCAAC ATTGCTAGTA TAAGTGCCCA	4320
CAAAATCCAA GTAAACATTA GTTCTTTTCT CCAATTTTCT CAATATAATC UATTTCTACC	4380
TTGTGCTCTC TCGGAAGAAC TGCTTCTGCC TCTAGATAGT CTAAATTTATC CATCAACCTT	4440
GCATCGTAAA TCCGAGATAG TTCCAACTTC ATCAGTTCAA TATCATATAA GCGTTTTCCT	4500
ATGTAAACAA TAATACCAA TCGTTTGAGG AATTGCTGCA CATCATAGAA TGTTTTCATA	4560
AGACTCATTC TAGCAAAATT TTGTGTTTTT TCAAGAAGA GACTCACACA ATGCTCTTTA	4620
TTTTCCTATC TTCTTAGCG ATTCTAAGGC AAGTATGGTA CAATAAAAAA ATGGGGATTCT	4680
AACAATTACA TT	4692

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 706 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

GCTAAAAAGC TGATAATCTT CGACTCCTGT ATATGATGTG TCTTTTCATG TAAGACACGC	60
GCCGCCACAA TCATGGCAAG AGCTGCAAGA CTGGCAAGTA AGAAGCCGAT AAGATAGCCA	120
AAAGATAAAG TCAATTTGAC AAAGAAAGTC AAAGAAGTA GGAACACAAA GCCTCCTCCA	180

1233

AAAACACCA	AAGTCTTTCG	TAAATCCCAG	ATTTTATCCA	ACTGCTTGAC	GAGGGAAGTC	240
GTCTGACGAA	CGCCTACAA	AGTTGCTAAC	ATACTTCCTA	AAAAGAATGG	ATAGACATGA	300
GTTAAACTGG	AGAAATAAAC	AGAGGAATAA	GAGGTCACTA	GAAAACTACC	AATAAACATG	360
GAGAAGAAAC	TGATCAAGAA	GGCAACAGCA	GATAAGAGAA	AGACCATCCU	CTTCAACTGA	420
CCATTGTGATT	TAGCTTGTTT	GGATAAGAAC	CAAACTGCCA	ATCCCCAAAG	AATATAGTAG	480
TGAACCTCAA	CTGCCAAACT	CCAATTATGA	ACAAACAAAT	GAGGAATGAA	CTGAGATTCA	540
TAACTCCAC	CTGTTAGGAG	TTCATAGAG	TTGGTCATAA	AGCCTAAGAC	GCCCGCAATC	600
TGCGCACCAA	TTCCAGCAAC	ATAGTCTTGG	CGAACCAAGA	AAGTAAAGG	CATGGTCACC	660
AAGACCATCA	AAACCACAGG	TGGCACAATC	TGATAAAAG	CGTCTT		706

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CAGCTGATGG	GCAATATCAG	TCATAGAAAT	TTTTCAATT	AACTTTTGAG	CAATTTTTTG	60
GTTGATGATA	CGAGGGAATT	GGTGAATTTT	CTTTACCAGG	GGAGTCTCAG	CAACCATCAT	120
TTTTGAACAG	TGATAGCACT	TGAACGGCG	TTTTCTAAGG	AGAATTCTAG	AAGGCATACC	180
AGTTGTTTCG	AGGTAGGGA	TCTTAGACGG	TTTTTGAAG	TCATATTCT	TCATTAGACT	240
TCCACAATCA	GGGCAAGATG	GAGCCTCATA	ATCCAGCTTA	GGGATAATT	CTTTGTGGGT	300
ATCCATATTG	ATGATATCTA	GAATCTTGAT	GTTTGGGTCT	TTAATATCGA	GCAGTTTTGT	360
GATAAATGT	AATTGTTCCA	TATGATCTTT	TCTAATGAGT	TGTTTTGTCG	CTTTTCATTA	420
TAGGTCATAT	GGGACTTTTT	TTCTACACAA	AAATAAGCTC	CATAATATCC	ATAGGGGATT	480
TACCCACTAC	AAATATTATA	GAGCCCGAAA	ATATGGGAAA	ACTGATCCTT	GTTTCTGCTT	540
TGTCTATAG	AAGAATAATA	AAGATTATCT	TCTTCAAAAT	CTCCGATATT	CTCTAAAGTT	600
TGTGCAAGT	TGCACAGAAC	TTGTTTATTT	TTTTGGTCA	CTTGCCATAG	AAATATAAAG	660
CGTTTCATA	TATAATATAA	TTATCAAAAG	ACAAAGGAG	TTACCTCAT	GGTGAATTTG	720
AATCTTAAAA	ATATTTACAA	AAAATATCCA	AACACGCAAC	ACTATTTCAGT	TGAAGATTTT	780
AACCTGAACA	TCAAAGATAA	AGAATTATC	GTTTTCGTAG	GACCTTCAGG	ATGTGGTAAA	840

1234

TCAACTACAC TCCGTATGAT TGCTGCTCTT GAAGACATTA CAGAAGGTAC TGCATCTATC	900
GATGGCGTAG TTCTCAACGA CGTAGCTCCA AAAGACCGTG ATATCGCCAT GGTATTCCAA	960
AACATCGCTC TTATCCACA CATGACTGTT TATGACAACA TGCGCTTCGG TTTGAAATTG	1020
CGTAAATACA GCAAGAAAGA CATTAAACAA CGTGTTCAAG AAGCAGCTGA AATACTTGGA	1080
TTGAAAGAA TCTTGGAACG TAACACGCTT GACCTTTTCAG CTGGTCAACG TCAACGTGTT	1140
GCCATGGGCG GTGCGATTGT CCGTAGTGG AAAGTATTCT TGATGGACGA ACCTTTGTCA	1200
AACCTGGATG CCAAACTTGG TGATCAATG CGTGTGAAA TCGCTAAAA TCACCGTCGT	1260
ATCGGAGCTA CAACTATCTA TGTAACTCAC GACCAACAG AAGCGATGAC ACTTGCAGAC	1320
CGTATCGTTA TTATGTGAGC TACTAAGAAC CCTGCTGTA CAGGTACTAT CGACGTGTA	1380
GAACAAATCG GTACTCCTCA AGAAGTTTAC AAAAATCCAG TPAACAAATT CGTTGCAGGA	1440
TTGATCGAGA GCCCAGCTAT GAACCTTCAT ACCGTGAAAT TGCTTGGTAG CGAAATTTGT	1500
TCGACGGT TCCGTTTGAAG ACTGCCAGAA GGAGCAATTGA AAGTCTCTCG TGAATAAGGC	1560
TACGAGGAA AAGAATTGAT CTTTGGTATC CGTCCAGAAG ACGTGAATGC AGAACCTGCT	1620
TTCTTTGAAA CATTCCCAGA CTGTGTTGTA AAAGCGACTA TCTCTGTATC AGAAGTCTT	1680
GGTTCAGAA CTCACCTTA CTGTCAAGTT GGTAAAGACG AGTTTGTTC AAAAGTTGAT	1740
GCTCGTGA CTCTGCAAC AGGTGCAACA GTTGAGCTTG GATTTGACTT GAACAAAGCA	1800
CACCTCTTCG ATGTAGAAAC TGAAAAAACA ATCTACTAAA ATAAATAAAA TTCAAAGCAC	1860
TACAAGAAA GATATCTCTT TATCAATTGT AGTGGAGAGA TATCAGTTAA TCTAGGAGAA	1920
GAAACAAAT GCTTCTCTCC TTTTGTCTAG AGAAGTCATA TTATGCATCT ATATTGTGAT	1980
GCTCTTTAAT ACTCTCGAA AATCTCTTCA AACCACGTCA ACGTCGCCCT GCCGTACGTA	2040
TGATTAAGTA TTTGCTCAGT TTTATCTGCA ACCTCAAAGA TGTACTTTGA GCAGCTTAGC	2100
GCTAGTTTCC TAGTTTGCTC TTTGATTTCC ATTGAGTATT ATTTGTGGGT ACCATCTACA	2160
AOTGAAGCTA TATGCGTAAA CTACGTGAGC AATTGAATTC GAAGTAGAGA GGTAAATAATA	2220
AATTTATGCT ATAGTTATGG TGAAGTGTAT GCTTTTGATG CTAGTTTATC AATAAATAGA	2280
TTAGAAATTG CAGATAATAT CATTTTGTGT TATTAATGAA AAAAACAAGA GTGTTTCAA	2340
TGTACAGAGC AGGTCAATAG TTTTACGAA AATTGGGAAA AAAACGCTTA CGTCCAGGTG	2400
GAAAGCTGC CACAGATTGG TTAATTGCAG AAGGAGGATT TTCAAAGAAA AAGGAAATAC	2460
TAGAGTTGCG GTGTAATAGG GGAAGTACAG CAATTGAGTT GGCACAGCCT TTTGTTGCA	2520
AGATAACTCG TGTGTATATG GATGCTCAAG CTTTAGAAGT GGCTAAAAAA TCTGCTGGAA	2580
CGGAGGTGT TGCTCATTTA ATCAGTTTGT AAAGACGAAA TGCAATGAAA CTTCCTTATC	2640

1235

AAGATGCTAG	TTTGTATAT	GTTATAAATG	AAGCTATGCT	GACTATGCAA	GCUGATCAAG	2700
CTAAGAAAAA	ATGTGTAATG	GAATATCTAA	GGGTATTAA	ACCTGGAGGT	CTTCTCTTGA	2760
CACATGATGT	GCTTCTTAAG	GAAGCTAAAG	AGTCTATCAG	ACAGGAATTA	TCACAAGCAA	2820
TTTCATGTAAA	TGTAGTGCTT	TTAACTCAAG	ATGGTTGGGA	ACAGGTGATG	ATAGAATCAG	2880
GTTATTGTGA	TGTGAAAGCA	TTGACTGGTG	AAATGACATT	AATGAAATTA	TCGGGTATGA	2940
TTTATGACGA	AGGTTTGCTA	GGAACTTTGA	AAATTGTGT	AAATGCTTGT	AAAAAGGAGA	3000
ATAGAAAGCA	GTTTTTAACT	ATGTATAAAA	TOTTTGCTAA	GAATAAACAG	AAMTTGGGCT	3060
TTATTGCGAT	GCCTAGTTAT	AAATCGTCAA	AACGTTAGAT	AATATTGAA	GTTAACTTTT	3120
CCCTTTTCTT	TTCTTAAAAA	ATATGCTATA	ATAGAGAGTA	AAAAACTTTG	AAAGAAAGAA	3180
AAAGATGAAT	TTAAAAGATT	ACATTTGCAAC	AATTGAAAAT	TATCCAAAGG	GTACCG	3236

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2885 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

CCTGACTTTT	CAAATTGGTT	AGTTTGCCAC	ACTTGGTTTA	TATGCTCGTG	GAAGCATGG	60
CTATTACTTC	TCAAAGGGCG	ATTTCTCACC	CCATGAAAAG	TGTCTATTTT	TGTTTGGGTT	120
TGTAAGTTAA	TTCAATTGTCA	CATATTACTC	TTTAACTGAT	TGAGTGAGTA	CCGCTTATAT	180
TTGATGCCAA	ACGCGCTAAA	AGTGTTACCC	TCAAGTCCTT	TTAGAATACG	GCTATAATTC	240
CGCTCATGTT	AACTATCTTT	ANGCTCATCA	CTATCTAGGT	TGGTATTAAA	AATGGTATTT	300
TCACGATGTT	TTAGCACGTC	AAAGAGTAAA	TCCTGCTCCC	AGTCACTCTT	AGGCTTAATA	360
ACAGCATTTT	TTGCTCTCAA	ATCATCAATA	ATTAAGTAA	CAACAGACTT	CATGAGTTCA	420
GTAGCTTCAA	ACTCTGTAA	TGTTGCACCT	TTACCATAAT	TCCACCCCTC	TTTAATTGTT	480
TTGATCATTT	CGGTTAGGCT	TACAAAAAGC	ACACTCTTAG	GTCTCTCTTT	TGCTTATAC	540
CCCTCATTTA	TACCTTTTGC	AATAGCAACT	GATAAAAGTG	TTTTCCTCAAT	CCCTGTACCT	600
CCGTGTATAA	GCATATTCC	CCTCATGCCA	TCAAGATATT	TTTGATACCTG	ACCTTTTGCA	660
AATTCATAAA	ATCCCTTTTC	TTCTGATGTT	ACAGCAATTA	AATCATCAAA	AGTTTTAGTT	720
TTAAACTCAT	CTGCTACATA	GCTCTTATTG	CTCATCAACA	CATTATAAGT	TTGCTATATAT	780

1236

AGTTTAGCAT	TCAAATTATC	AGCAATCGCA	TCPTCTTCAT	CTTGCTTTTT	CTGPTCTTCT	840
TGGCATTTGT	CACAAATAGG	TGGGATACAG	CGAACTTCTT	TTAATTGCCTC	TCGGTCTCTA	900
TTCCACCCCA	CTACTACATG	TCTTCTCCT	TGATTTGTG	TTAGCTGTAT	TTCATGCTTA	960
GGACACAATT	CGCTAGATT	AAATGTCCTA	ATATTTCTTA	AACATGATG	TAATGATTTC	1020
ATTTTCTGAC	CTCCAAAAT	GGTTTTCTT	GGTTGGTAT	CCAAATCTCA	TAGCTGGTAG	1080
GCTCTAGTTG	ATTGGTTTGC	TGTTTTTTAG	CCTCACGCGC	TGCCCTGCTA	TTTCTAACAA	1140
GTCCACCGGT	CAATAAATTG	TCCTGTTTCC	AACGGTTAAG	GATTAACCTG	ATGTATGCAA	1200
AGTTTGCTTT	ACCCTGACTG	ACAGCCTCTT	TTAACGCCCTC	ATGGATAAGC	TCTGGGCTAA	1260
AATCTTCTAG	CATATACTGC	AATTCCTGAA	TCGTTAACGG	TGACAAATGCT	TTACCTGTCT	1320
CAGCTCGCTT	CATATTCAAC	AAGTCGTCTA	TTTCCACACT	GGTTACTTTT	TTATTACAAA	1380
AATCAGAAAT	CAGTTGAAAA	ATGTTTGGAC	TTTGTAGCTG	GATTTCAGCC	ATTACCTCMT	1440
CAAAATCTCG	TGTGTGCATG	TGTCTAAAT	CTAGTGTCTA	TGCAATGCCT	CCTCAAACTT	1500
CTCTATAAGA	CAACTTTTAT	TTGCTTTCTG	AGTTCCATT	TTAGAGTTAA	AAAGAAATATC	1560
TTTAAAGGTT	ACAGTAGCCT	CTAANTACTC	CTTTTCAGCA	TGCTCTATAT	ACGCGTGTG	1620
CTCTGCTTCG	TTCTCAAAA	AGTGCTTAGC	TTGGCGTTTA	AAGAATGCTT	TTCCGATPAGC	1680
GTCCATTCTCA	AAAATACCAG	GGCGGAAAA	CATTCCCGTA	GTGCTTTTAG	AGACCGCTTC	1740
GATTTTATGG	CTTTCATTCA	ATTCAGGAAG	TTCAAATCCAA	AGTAAACGGG	ACAACCTATC	1800
TTTGATGGAT	TTTGTCTGAC	TTTCCAAATA	AGAAAGGATT	CTTAGGCCAT	TTTCTTCGCT	1860
AAATTTCTCG	ATTCTGCGC	TAAATCTGTC	TATACGTCTA	GTTAATAATCT	CATATGTTGT	1920
TTCTGTCAAT	TTTTTACCTC	TGTTTCTTTG	TTGGTGTGAT	TTTTTTAGCTT	ATTTTTTTTAC	1980
TTCTAAACAT	CATTGTCTTA	ATTTCTTGAT	AACATATTTT	CAATTCAATC	ATAGCTATTG	2040
CCATATCCTC	AAATGCGCTG	TACTGTCTCA	ACTCCTCACT	AGTCAAGCTA	TCGATACCGT	2100
TATAGCCCCC	ACGCTCTTCT	CTTAACCTGT	TAGCGTTTAT	GTCTGTACT	GCCTTTAGTA	2160
GCAAGTTGTT	CATGGTGCTA	TGCGCGTGCT	TTGGTGCAAT	AGGCCATGTT	TCTATACTGT	2220
CATGCAAGGT	TTTTCTTTTC	GGTTTTTCTA	CGGCCCTCTG	CAGACGAATT	TCAGAAAGTT	2280
CCTCACCGAT	TTCAAGAAAT	GCTTTGACTA	GGTTTAGTTT	GAATTCGCGT	ACTGTTTCGG	2340
TATTTCTTAA	ATAAGTGATC	AGAAAAGTAG	CCTGTGCTC	GTTCAGAAATA	TAGGATTTTT	2400
TAGGTGTGCC	TCTAGTATCT	AATTTATGGA	TTTTAAATCC	AAGTATTCCC	AACTCTTCAA	2460
AGTCAGCCTT	ATTTTCTCTT	ATTAAGCGCG	TGATAGTGTG	GTGTTGTACT	TCAGCACATT	2520
CAGCGATGAT	CTCGCTTGTG	GTGTACGGCT	CTTTCTTACC	GTCCATGTAA	ACTAGTTCCA	2580

1237

TTACGGTTCT ACCTCCTGTA TAAATCTGGT TAGCTTACTT TTTAATGGCC TCCTCTAGCC	2640
TCCTTTTITAG CCTCTAAAC GGCTTGGCT AGTGGTTAAT ATTATTACC ACTTGTCTCT	2700
ATTAACGTGT TAGAGGCTT TATAACGACT TGATCGCTG TATCGATATC CTCGTGGAA	2760
TAGTAGATTT ATTTTCTAAT ATCATCTAAG ACTTGTTTAA CCCATTCTCT GAAAGAAATA	2820
AAATPACATC TTCTTTATCC TTGGCATCTG CTTTGTCTGA GACAAATTAG AATGTCAATA	2880
CTTGG	2885

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

TATCAATCTT TTCCATTAT AGGAGCAACA GAGTGGGAGT AGTCATCAA GGACTAATTT	60
ATGTATTTT ACGAGTCAGT ATCTGGGAGT ACTGGTTTTT ACTTTCTAG ACTTTTGAC	120
TACTGTGTAA AACGGGATA ATTTTCGACT GTTAAACAGT TATTATGCAA AGTCTAAAAG	180
ATTAGAAATG TCAAAACAAT CCGCTAGGC TTGATTTTAT CCTTTATTTA CTATAAAATG	240
AGAAGGAAAA ATGTCAAAC TTTATATTGC AATAGGAGA AATCATGACA AAAACATTAA	300
AACGTCTGTA GGTTTTATCA CCTGCAGGGA CTTTAGAGAA GCTAAAGTA GCTGTTCAGT	360
ATGGAGCAGA TGCTGTCTTT ATCGGTGGTC AGGCCTATGG TCTCTGTAGC CGTGGGGAA	420
ACTTTACTTT CGAACAGATG GAAGAAGGCG TGCAGTTTGC GGCCAAATAT GGTGCCAAGG	480
TCTATGTAGC GGCTAATATG GTTATGCACG AAGGAAATCA AGCTGGTGCT GGTGAGTGGT	540
TCCTGAAACT CGGTGATATC GGGATTGCAG CAGTTATCGT ATCTGACCCA GCTTGAATTA	600
TGATTGCAGT GACTGAAGCA CCAGGCCTTG AAATCCACCT TTCTACCCAA GCCAGTGCCA	660
CTAACATGTA AACCTTTGAG TTCTGGAAAG AGCTAGGCTT GACTCGTGTC GTTTTAGGCG	720
GTGAGGTTC AATGGAAGAA TTAGCTGAGA TCCGCAACG TACAGATGTT GAAATTGAAG	780
CCTTTGTCCA TGAGAGTATG TGATTTTCAT ACTCTGGAGC TTGTACTCTT TCAAACCA	840
TGAGTATGCG TGATGCCAAC CGTGGTGGAT GTTCTCAGCT ATGCCGTGGG AAATACGACC	900
TTTACGATAT GCCATTGGG AAAGAAGCTA AGAGTTGCA GGGTGAGATT CCAGAGAAT	960
TTTCAATGTC AGCCGTGAY ATGTCTATGA TTGACCACAT TCCAGATATG ATTGAAAAAT	1020

1238	
CTGTGGACAG TCTAAAAATC GAAGGACGTA TGTAGTCTAT TCACTAyGTA TCAACAGTAA	1080
CCAACTGCTA CAAGGCGGCT GTGGATGCCA ATCTTGAAAG TCCTGAAAAG TTTGAAGCTA	1140
TCAAAACAAGA CTTGTGGAC GAGATGTGGA AGGTTGCCCA ACGTGAAC TGCTACAGGAT	1200
TTTACTATGG TACACCATCT GAAATGAGC AGTGTGTTGG TGCTCGTCGT AAAATCCCTG	1260
AGTACAAAGT TGTGCTGAA GTGTTTCTT ATGATGATGC GGCACAAACA GCAACTATTG	1320
GTCAACGAAA CGTCATTAAAC GAAGGGGACC AAGTTGAGTT TTATGOTCCA GGTITCCGTC	1380
ATTTTGAAAC CTATATTGAA GATTTCGATG ATGCTAAAGG CAATAAAATC GACCGCGCTC	1440
CAAAATCAAT GGAACATATG ACTATTAAAG TCCCAACAAC TGTTCAATCA GGAGACATGG	1500
TTGAGCTCTT TAAAGAGGGG CTTATCAATC TTTATAAGGA AGATGGAACC AGCGTCACAG	1560
TTGCTGCTTA ATGTAGTTGT TTAGTTTTAA AAAACTATGC AAAGCTCCAT ATACAACACT	1620
TAAACGAGAT TAAAGAATGG CGAAATCCCT TGATGCGCAA GAGATTAGCT GTCTTTTTTA	1680
TTTTTTAAGT GATAAAGTCG GAGTTTAGGC ATCAAAGCCT ATCAAATTAA ACAAGAAGCA	1740
GATGTCTTAG ATATTGTGA AAAAATTAAT AAGCAGAAAA CTCTCTATTA TTTGTGTTGA	1800
GAGAGTTTTT TGTTAATAAA ATTTACAAA ATGACATTTA TATATTGCAT TAAGTTAGAT	1860
ATATGATATA ATATTGTAA AAAGAGGCGC AACTTTTTAA AATTAAATGAG AATCAAAGAG	1920
AAAACCAATA ATATTAATGG AGGAATAAAA AATGTAAATA AGCATTATGG TCATTCAATC	1980
ATTCTCAAAG ATATAAAATTT TGCACCTAAC AAGGGTGAAA TTGTTGGTCT AGCAGGGAGA	2040
AATGGAATTT GTAAGATAC GTTGATGAAA ATTCCTGTTT AGAATAATCA ACCGACTTCA	2100
GGTAATATTA TAAGCAGTGA TAATGTTGGG TAATTAATCG AAGAACCAAA ATTATTTTTA	2160
TCTAAACAG GTTAGAGAA TTTAAATAT TTGTCAAATT TATATGGTGT TGACTACAAT	2220
CAAGAAAGAT TTAGATGTTT GATCCAAGAG TTAGATTGGA CTCAGTCTAT TAATAAAAAA	2280
GTAAAGACCT ATTCTTTGGG TACAAAACAA AAATTAGCTT TGCTTCTAAC TCCTGTTACG	2340
GAACCTGATA TATTGATTTT AGATGAACCG ACTAATGGTT TAGATATTGA ATCATCACAA	2400
ATAGTTTTAG CGTTCTTAAA AAAATTAGCT TTACATGAAA ATGTGGGAAT TTTAATATCG	2460
AGTCATAAAT TAGAAGACAT TGAAGAAATT TGTGAGAGAG TTCTTTTCTT GGAGAACGGG	2520
CTTTTGACAT TTCAAAAAGT AGGAAAAGAT AGTCATAATT TCTTGTTTGA GATAGCTTTT	2580
TCATCAGCTA CAGATAGAGA CATTTTCATT ACCAAACAAG AATTTTGGGA TATTGTTTAG	2640
GANGAGGGAT TGAGAAATAC TATGTCGGG AATATTCAAA ATAGTGAGCT TTTTAAATTT	2700
TTTAAAGAAA ACTCTATTAA AGTAGTTGAT TTGAAACTA AAAAAGAGAC GCTTAAAGAT	2760
ATTTACCTAA ATCTTCAA AATAAGGAAG GTTATAATCA TGAAATTAAT TAAACAGAAG	2820

1239

AATCGGATGA TTTACGTCCT GTCTAATTTT CTATATGCTA TCTCAGTTTC CATTATTTAT	2880
GCTTTGAATG GCATTGTGTT ACTAGTCATA GTAAAGTAAT TGGCTATTCC AGTGATTTTA	2940
GGATTAAATF TTATAGTAGC TATTGTAGTC AATACAATTT TGTTAGTCCT GTTTTATTTT	3000
CTATTATCTT ACATTTTCTA TTTATACAAA TTGAAAAGTG GCTTGGTATF TGGTATTTTA	3060
GTAGCTTTAC TACTCTTTAT CTCTAATATA TTAATACGA TGATGATGAA TACTAGTAAT	3120
GATTTGTTTA TCAAAGCAAT TGAA	3144

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3756 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TACGGTATTA TTTTAAAGG AAGAGAAATCA TGAATAATCA AAAATGGCTT GGTCTAGCAG	60
CCCTTGCTAC AGTCGACAGT TTGGCTCTTG CAGCTTGGCG AAATCAGAA AAGAAAGCAG	120
ACAATGCAAC AACTATCAAA ATCGCAACTG TTAACCGTAG CGGTCTGAA GAAAAACGTT	180
GGGACAAAAT CCAAGAAATTG GTTAAAAAAG ACGGAATTAC CTTGGAATTT ACAGAGTTCA	240
CAGACTACTC ACAACCAAAC AAAGCAACTG CTGATGGCGA AGTAGATTTG AACGCTTTCC	300
AACACTATAA CTCTCTGAAC AACTGGAACA AAGAAAACGG AAAAGACCTT GTAGCGATTG	360
CAGATACTTA CATCTCTCCA ATCCGCTCTT ACTCAGGTTT GAATGGAAGT GCCAACAAAGT	420
ACACTAAAGT AGAAGCATC CCAGCAAAAG GAGAAATCCG TGTACCGAAT GACGTACAA	480
ACGAAAGCCG TGCGCTTTAT TTGCTTCAAT CAGCTGGCTT GATTAAATTG GATGTTTCTG	540
GAACTGCTCT TGCAACAGTT GCCAACATCA AAGAAAATCC AAAGAACCTG AAAATCACTG	600
AATTGGAGCG TAGCCAACA GCTCGTTCAT TGTCTCAGT TGACGCTGCC GTTGTAACA	660
ATACCTTCGT TACAGAAACA AATTGGACT ACAAGAAATC ACTTTTCAA GAACAAGCTG	720
ATGAAAACCT AAAACAATG TACAACATCA TTGTGCAAA AAAGATTGG GAAACATCAC	780
CTAAGCTGTA TGCTATCAAG AAAGTAATCG CAGCTTACCA CACAGATGAC GTGAAAAAAG	840
TTATCGAAGA ATCATCAGAT GGTITGGATC AACCGATTG GTAATAAGAA ACAGGAGAGT	900
GGGAGAGAAA ATTCCACCTC TTGCTTTTGT ATAGATATA GATTGTAAG AAGACTATTG	960
GTTCATAGAA AGGTAGAGAG AATATGTTTT TTCTAGCGA ACAAGAACAG ATTGAAAAAT	1020

1240

TTGAAAAGGA TCATGTAGCC CAGCATTTATT TTGAGGTTTT GCGTACCTTG ATTTCTAAGA	1080
AATCAAGTCTT TGCCACAGCAG GTTGGACTCA AGGAAGTCGC AATTTATCTG GGTGAGATT	1140
TCAAGCGTGT TGGAGCTGAA GTGGAGATTG ATGAGAGCTA TACAGCGCCC TTGTCTATGG	1200
CACATTTCAA GAGTTCGGT CCAGATGCCA AGACCTTGAT TTCTCTATAAC CACTATGACA	1260
CTGTGCCAGC GGATGGGAT CAGGTCTGGA CAGAGGATCC ATTTACGCTT TCGGTCCGCA	1320
ATGGCTTCAT GTATGGGCGT GGGGTGTATG ACGACAAGGG TCATATCACA GCTCGCTTGA	1380
GTGCTTTGAG AAAATATATG CAGCACCATG ATGATTTACC TGTCATATTC AGCTTTATCA	1440
TGGAGGGAGC GGAGGAATCG GCTTCAACAG ACCTAGATAA GTATTTGGAA ANGATGCGAG	1500
ACAAATCTCG TGGGGCGGAT TTGTTGGTCT GGGACAAGG GACCAAAAT GCCTTGGAAC	1560
AGCTGGAAT TTCTGTGGC AATAAGGGGA TTGTGACCTT TGATGCCAAG GTAAAAAGCG	1620
CTGATGTGGA TATCCACTCG AGTTATGGTG GTGTGTGGGA ATCAGCTCCT TGGTATCTCC	1680
TCCAAGCCTT ACAGTCTCTT CGTGTGCGG ATGGCGGTAT CTTGTTGAA GGCCTGTAGC	1740
AAGAAGTACA AGAGCCCAAT GAACGAGAAA TGGCCTTGCT AGAACTTAT GTCAACGAA	1800
ACCCAGAGGA AGTTAGTCGG ATTTATGGAT TGGAGTTGCC TCTCTACAG GAGGAGCGGA	1860
TGGCCTTTCT AAAACGTTTC TTTTTCGATC CAGCGCTTAA TATCGAAGGA ATCCAGTCTG	1920
GTATATCAAG TCAGGGTGT AAGACTATT TACCTGCAGA AGCAGTGCC AAGCTAGAGG	1980
TTGCTCTGTT TCCGGGCGTA GAACGCGATG ATGTTCTGGA AAAAATTGG AAACAGCTAG	2040
ACAAAAATGG CTTTGTAAAG GTAGAATTAT ACTATACCTT GGGAGAGATG AGCTATCGAA	2100
CGGATATGAG CGCACCGACC ATTCTCAATG TGATCGAGTT GGCCAAGAAA TTCTATCCAC	2160
AGGGCCTTTC AGTCTTGCCG ACGACAGCGG GGACAGGACC TATGCATACG GTCTTTGATG	2220
CCCTAGAGGT ACCAATGTT GCATTGCGTC TAGGAAATGC CAATAGCGGA GACCACGGTG	2280
GAGATGAAAA TGTGCGAATC GCTGATTATT ACACCATAT CGAATTAGTA GAGGAGCTGA	2340
TTAGAAGCTA TGAGTAGAGA TATTATCAAG TTAGATCAGA TCGATGTGAC TTTTCACCA	2400
AAGAAGAGAA CCATCACAGC GGTAAAGGAT GTGACCATCT ACATCCAAGA AGGGGATATC	2460
TACGGAATCG TTGATATTC TGGAGCAGGA AAATCAACCC TTGTACGGGT GATTAACTCT	2520
TTGCAAAAAC CATCTGCAGG GAAATTTACC ATTGACGACG ATGTGATTTT TGACGGCAAG	2580
GTGACCTTGA CGCGAGACGA GTTGCGTGT AAACGTCAAG ATATCGGAAT GATTTTCAG	2640
CATTTTAACC TGATGAGCCA AAAGACAGCA GAGGAGAATG TAGCCTTTGC CCTTAAACAC	2700
TCCTGAACCTA GCAAGGAAGA AAAGAAGGCT AAAGTAGCTA AGTTGTGGGA CTTGTTGTGT	2760
TTGGCAGATC GTGCTGAAA CTACCCCTCA CAACTATCTG GAGGGCAAAA ACAGCGTGTG	2820

1241

GCAATTGCGC GFGCCTTGGC CAATGATCCA AAAATCTTGA TTTCAGACGA GTCAACTCTT	2880
GCCCTTGATC CGAAGACAAC CAAGCAGATT TTGGCCTTGT TGCAGATT TTGAACAAAA	2940
TTAGGCTTGA CTGTGTCTTT GATTACGCAT GAAATGCAGA TTGTCAAAGA CATTGCCAAC	3000
CGTGTGCGAG TTATGCAGGA TGGGCATTTG ATTGAAGAGG GTAGTGTGCT TGAATCTTTC	3060
TCAAACCCTA AACAACTTT GACTCAAGAC TTATCTCAA CAGCTACAGG TATTGACGAA	3120
GCCATGGTCA AAATCGAGAA GCAAGAAATC GTGGACACT GTCTGAAAA CAGTCTCTTG	3180
GTGCACTCA AGTACGCTGG AGCTTCAACA GACGAGCCAC TTTTGAATGA ATTGTACAAG	3240
CATTACCAAG TAATGGCTAA TATTCTCTAT GGAATATCG AAATCTCGA TGGTACTCCT	3300
GTGGAGAA TTGTGGTGGT TTTGTCAAGT GAAAAAGCAG CGTTGGCAGG TGCCCAAGAA	3360
GCCATTGCTC AAGCAGGTGT ACAACTAAAA GTATGAAGG GAGTACAGTA AGATGGAATC	3420
ATTGATTCAA ACCATTATAC CAAATOTCTA TAAGATGGGT TGGGCTGGTC AGGCAGGCTG	3480
GGGAACGGCT ATCTACTTAA CTCCTTATAT GACAGTTCTT TCCTTCATTA TCGAGGCGTT	3540
CTTGGGGCTA GTGGCAGGTC TCTTCTCGT CTTGACAGC CCAGTGGTG TCTTGGAGAA	3600
TAAAGTCGTA TTCTGGATT TAGACAAAA TACCTCAATT TTTCGTGGG TTCCCTTTAT	3660
CATCCTCTTG GCAATCTTGT CACCACCTTC TCACCTGATT GTTAAAAACA GTATCGGGCC	3720
AAATGCAGCC CTGTGCCAC TTTCTTTTGC AGTCTTTGCC TTCTGG	3766

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TGTGCTGAG TTAATCGGTA CGTTCATGTT TGTATTGCT GGGACGAGG CTGTGTGTTT	60
TGGAATGGT CTGTATGGCC TTGGTCACCT TGGAAATGCC TTTGCCCTTG GTTTGGCAAT	120
CGTGGTGGCA GCCTACTCAA TCGGAATGT TTCAGGTGCT CACTTGAAC CGGCTGTTTC	180
GATTGCTATG TTTGTAAACA AACGTTGTG ATCTTCAGAA CTGTGAACT ACATCCTTGG	240
TCAGTTGTGT GGAGCTTTCA TCGCTTCTGG CGCTGCTTC TTCTCTTGG CTAACCTCAG	300
TATGTCAACT GCTAGTCTTG GTGAAAATCG CTTGGCAAC GGTGTCACTG TCTTTGGTGG	360
TTTCTGTGTT GAAGTCATCG CAACTTCTT GTTTGTATTG GTTATCATGA CTGTGACTTC	420

1242

AGAAAGCAAG	GCAGTGGCG	CGATTGCTGG	TTTGGTAATC	GGTTTGTCAT	TGATGGCGAT	480
GATTTCTGTC	GGATTGAAGA	TTACTGGACT	TTCACTAAAC	CCAGTCTGTA	GCTTGGCACC	540
AGCTGTCCTG	GTAGGGGGCG	CAGCTTCAA	CAAGTTTGGG	TTTTCTATCT	TGCACCAATC	600
GCTGGTGGAG	TTCTTGCAGC	CTTTGGTGCA	AAAAATTTCC	TTGGGAACAGA	AGAATAATPG	660
AAACTCAAAA	AGCCTTGCCT	CTCATCTTGA	GGACACGGCG	TTTTTTCGTAT	GATACCTCTC	720
GMAATCTCT	TCAAACACAG	TCAGCTTCAT	CTTGGCGTAG	TATGGTTACT	GACTTCGTCA	780
GTTCATATCCA	CAACCTCAAA	ACAGTGTFFF	GATCTGACTT	CGTCAGTTCT	ATCTGCAACC	840
TCAAAACAGT	GTFTTAAGCT	GACTTCGTCA	GTTCATATCTG	CAACCTCAAA	ACAGTGTFFF	900
AAGCTGACTT	CGTCAGTTCT	ATCTGCAACC	TCAAAACAGT	GTFTTAAGCT	GACTTCGTCA	960
GTTCATATCTG	CAACCTCAAA	ACAGTGTFFF	AAGCTGACTT	CGTCAGTTCT	ATCCACAACC	1020
TCAAAACAGT	GTFTTAAGCT	GACTTCGTCA	GTTCATATCCA	CAACCTCAAA	ACAGTGTFFF	1080
GATCTGACTT	CGTCAGTTCT	ATCCACAACC	TCAAAACAGT	GCTTTGAGCA	ACC TGCGGCT	1140
AACCTTCCTAG	TTTGCTCTTT	GATTTTCATT	GAGTATGACT	TTAGCGGTGG	TCAATTTTCT	1200
CTGGATAAAG	GTGGTGTGG	AAGAGGCGTT	GTTCGCGCAA	GCCTTCATAC	TTAGTCTCTT	1260
GCTTACCGTA	GTGTGTAGTAG	GGGTGGATTG	AAATGCCACC	GC GCGGAGTG	AAATTTCCCC	1320
AGACTCTTAA	ATAGCGAGGG	TCTAGCAAGT	TGACCAAGTC	TTTCCCGATG	GTGTGTATAC	1380
AGTTTTCGTG	GAAATCTCCG	TGTTTTCGGT	AGCTAAATAG	ATATAGTTTG	ACGATTTTGG	1440
ACTCGACACA	GAGCTTGTCA	GGAAATGTAG	AAATATGAAT	CGTCGCAAG	TCTGGCTGAG	1500
CAGTATTTTG	TCCCAGCAGA	GACATATCGA	GGATATGGTG	ACGAATGCC	TGTTCCTTAG	1560
CGATTTCTCT	AGTAATTTGA	ATTTGAGGT	GATGACGTTG	GCCGTAGGCA	AAGGTGACAG	1620
CTTCGACTGT	TTCATAGTGT	TGCATGACCC	AGAAAAGGCA	GGTTGTTGAA	TCTTGACCAC	1680
CACATAAGAC	GACCAAGGCT	AAATGACGTT	TCTATAGTACT	CCTTCCAAAA	TGGGAATGTT	1740
TCAGAGCAGC	CAAAAAGCTC	CCATTAGGGA	GCTAAAAAAT	ACCAAAATCGA	GGTTTTTTTA	1800
GCAGTGGCAT	ATCCCAAACA	TCGTAATATT	CTACTTATAT	AGTAAAATGA	AATAAGAACA	1860
GGACAAATCG	ATCAGGACAG	TCAAATCGAT	TTCTAACAAT	GTTTTGAAG	TAGAGGTGTA	1920
CTATTTCTAGT	TTCAATCTAC	TATAGTCTAG	CATATTTTTT	GAATAATGGC	AAAGGGCAAG	1980
AAAAAGAGA	CCAAAGAAAG	TACTTGGTCT	CTCGTTTGAT	TAGCTCAATT	CAGCAATGAT	2040
GGCTTGATTT	TGTTCTGCTG	TGTGAACACC	TGCAACTGTG	TTGACAACTT	GGCCGCTTTT	2100
TTTGAAGAGA	AGAGTTGGAA	TAGACATGAT	TCCAAAAGCA	CGAGCTGTGT	TTGCAATTTT	2160
ATCAACGTCC	ATTTTAACGA	TTTTCAAGAC	ATCTTCTGAA	AGTTCTTCAG	ACAATTTGTC	2220

1243

CAAGATTGGA	CCTTGCATAC	GACATGGACC	ACACCAAGTT	GCCCGAAGT	CTACTAAGAC	2280
CAAAACCGTCT	TTTGTTCCTT	GTCGAATGT	TGCATCTGTA	ATTGCTTTTG	CCATTGTGATT	2340
TCTCTCTTTT	TTAGTTATAT	TGGCTTAAAT	CTTGTTTCAT	GAGATAGAAG	AAGATATCTC	2400
CATAAGTCCC	ATGGTAGTCC	AAATATGAC	CCTTGTAAAT	TAAATTTTGG	ACAGGGTAGT	2460
AkkCTGCGAC	GCGGATAAGG	CAAGCTTGTT	GCGAACGTT	AAAGTCTTCA	TAAGACTCGG	2520

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

ACTCAGTTAG	ATTTTGTTTT	CAAAACAAC	GAAGAAAG	ACCATGTTGC	TCTACTTGGA	60
AGAATTGGCT	CCGAACGCTT	TTATCGATAT	ATTATATAAA	AATATTTAGA	TTTACCGGAA	120
ACATTGAAA	ATTATAATGT	TTTTGTACCA	GAAGCTAATG	GAAGTGGTGC	CTTAGGTGAA	180
GTCTTATCAA	CACCCCTAAT	CGGGGAACCC	CTAATCGGGC	ATACAGATAC	TTTTTTATCT	240
ATTGTAATT	TTAAACAAA	ATTTGAAGCC	GATGCTGTGA	TTAAATTTAT	TAAAACTAAA	300
TTGGGTAGAG	TATTATFAGG	TGTTTTGAAA	GTACTCAGC	ATAATTCACG	CAAAACTTGG	360
TATTACGTCC	CCCTCCAAGA	CTTTACGGTC	AATCGGACA	TTGATTGGAC	ACAATCAGTG	420
ACTGATATTG	ACCGCCAGCT	TGATCAAAAA	TATGACTTTT	CCCTTGAAGA	AATTCGCTTT	480
ATTGAGAATC	ATGTAAAGGA	GATGGATTAG	AAAAGTATTT	TTATTTGACA	AATAGTGCTC	540
AATGATCTAA	AATGACTATA	TAGGATTAGG	TCAGGAAGCA	TACGATGCCC	TGACCTTTT	600
TGTACTTATG	AGATGAGAAA	GTCATTTGTT	AGATAAATTG	ACTCGTTAGC	AAAGTTTCAA	660
AAAAGGAAA	CTTATGCCAG	TAGAAATTAA	AACCACTAAA	GAAATTCATC	CTAAATCTTA	720
TGCTACACCC	ACACCGACAG	TAACCGAGTA	TGAAGCTGG	ATTAAAGATTG	GGTATACAGA	780
ACGTGATGTC	ACACAACGTA	TCAAGGAGCA	AACGCATACA	GCTCATATAG	CTACAGATGT	840
CTTATGGACT	GGTGATCGAG	CTTATACAGA	AGAGCCTGAT	AAGGGGAAAA	CTTTCAAGGA	900
CCATGATTTT	CACCAATTCC	TTTCTTTCCA	TGATGTAGAA	CGTCGTCCCA	AGACGGAATG	960
GTTCATTTTT	AATGGAACTC	CTGAAAAATC	AAAAAATCTT	TTTGATAAGT	TTGTTTACGA	1020
TGATTTGTCT	GGTTATCAGC	CTGAAAAAGG	ACAGGACTAT	ACTCTGCGAC	AAGAGCAAGA	1080

1244

AGAAGCAGTT GCTAAGACAT TAGCTTATTT CCAAGAACAT GCTGGAGCCA AGTTCTCTGT	1140
GAATGCCAAG CCACGCTTTG GTAAAACTTT GTCTACCTAT GACCTAGCTC GACGGATGGA	1200
AGCTGTCAAT GTCTAATTG TAACAAACCG CCTGCCMTT GCTAACTCAT GGTATGATGA	1260
TTTTGAAACA TTCAATAGCAG GTCAAAACGAC TTACAAGTTT GTTCTGAAT CAGATAGCCT	1320
TAAGAGTCTT CCAATCTTGT CACGACAAGA ATTTCTTGGT ATTTTAGCTG ACGATGTAAG	1380
ACAACCTGCT TTATACAGTC TCCAAGACTT GAAAGGATCT GTTTATTTAG GTGGAGAGCA	1440
CGATAAACTC AAATGGGTAA CTGATCTGCA TTGGGACTTG TTGGTTATTG ACGAGGCTCA	1500
TGAAGGAGTT GATACCTTCA AGACTGACCA AGCCTTTAAT AAGATTCGAC GAAATTTTAC	1560
CTGTGATTTG TCAGGTACAT CATTTAAAGC ATTTGGCTAA GGAGATTTTA CAGAGGAACA	1620
AATCTACAAC TGGTCTTATG CTGATGAGCA GGCTGCTAAG TATTCTGTGT CTCTTGAGCA	1680
AGAAGAGGAA AATCCTTATG AAAGCTTGCC TCAGTTGAAT CTCTTTACCT ATCAATGTCT	1740
TCAGATGATT GCGGAAAGT TAGAAAAAGG CGCTCAGATC GATGTGAAAT ATATTGACTA	1800
TGTTTTTTGAC TTAAGTGAAT TTTTCGCTAC AGATGATAAA GCGAAATTTA TTCAATGAGCA	1860
TGATGTCAGA AATTGGTTAG ATACTCTATC AAGCAATGAA AAATATCCAT TTTCAACCAA	1920
AGAATCCCTT AATGAACCTA AGCATACTTT TTGGCTTTTA GAACGTGTG CTTCGGCCAA	1980
AGCATTTAAA GCCCTACTAG AAGAACACCC AATCTATGAA AACTATGAGA TCGTTCTAGC	2040
TGCTGGTGAC GGACGTATGT CCGAAGAAGA CGATAAAGTC AAATCAAAAT CCTTGGACTT	2100
GGTTAGAAAA GCGATAGCAG AGAATGACAA AACCATTACC CTATCCGTTG GTCAGCTGAC	2160
GACAGGTGTC ACTATCCCTG AATGGACAGG TGTATTGATG TTATCAAAAT TGAATCACC	2220
AGCTCTTTAT ATGCAGGCCG CCTTCCGTGC TCAAAATCCT TACTCATGGA GCGATAACAA	2280
AGGAAATCAC TTTTCGCAAG AAAGAGCCTA TGTATTTGAC TTTTCGCCGG AAAGAACCTT	2340
GATTCTCTTT GATGAGTTTG CCAACAACCT ATTGCTTGTA ACTGCAGCTG GTAGAGGAAC	2400
TTCACTTACA CCGCAAGAAA ATATTAGAGA ATTATTAAAC TTCTTTCCAA TTATTGCCAA	2460
AGACCGTGCT GGTAAAGATGG TTGAAATTGA TGCAAAAGCA GTTCTAACCA CTCTCGCCCA	2520
GATAAAAGCT AGAGAAAGTC TTAACGAGG TTTTATGTC CCAATCTTAT TTGATAATAT	2580
TAGTGTGATT TTCCAAACAA GTCAAAACAGT TTTAGATATT TTAATGAGC TGCCAGTTGA	2640
AAAGGAAGGG AAGGTACAAAG ATAGTTCTGA TTTTATGAT TTTTCAGATG TTACAGTCGA	2700
TGATGAGOGA AATGCAGTAG TAGACCATGA AATTGTAGTT AATCAGCAAA TCGCACTTTT	2760
TGTTGAAAAA GTTTATGGAC TTGGTGAATC TGTGCTGAG TTATGTCACAA AAGATGAGGA	2820
ACGAATCTCA AAACAGCTGG TCAATGACTT GAGTAAGACC GTTCTTTCAG TGATTGTAGA	2880

1245

GGAAATTGAAA	GCAGATTATT	CTCTAAAAAC	AAGGGAACT	GAGCAAAATTA	AGAAAACAAT	2940
TACAGCAACA	CTTGAGAAATG	AAATTCGAAA	AAATGATATC	GAAAGAAAAA	TTTCTGAAGC	3000
TCATATCAAG	CAAGAGTTGC	AACAGCAGCT	CAAGAAGCA	AATGATAAAG	CGCAAAAAGA	3060
TAAGATTCAA	GAAGATTGG	AAAAACGTTT	AGAAGAAAT	AACTCATTC	ATAAAGAAAA	3120
ACTAGAACAA	ACACTCAAAA	AAGAAAGTGA	AAAAATGCCCT	GAGAAATTTA	TCGAACAGGT	3180
TGAGATAAAA	CGTGIGGAAC	AGTTGAAACA	ATCAGCTCAA	GATGAAATTC	GTGACCATTT	3240
ACGAGGGTTT	GCAAGAACAA	TTCCAAAGTTT	TATTATGGCT	TACGGTGATC	AAACTCTAAC	3300
ACTTGATAAT	TTTGATGCCCT	TGTTTCCTGA	ACATGTTTTT	TATGAAGTAA	CAGGGATTAC	3360
GATTGATCAG	TTTAGATATT	TGCGAGATGG	TGGGCAGGAT	TTTGCAGGGC	ATCTCTTTGA	3420
TAJAGCAACA	TTTGACGAAG	CTATTCAAGA	ATTTCTTGGC	AAGAAAAAGG	AGTTGGCGGA	3480
TTATTTTAAA	GATCAAAAAG	AAGACATTTT	TGACTATATT	CCACCCGAGA	AGACCACCA	3540
AATTTTCACT	CCTAAACGAG	TGGTGAAAAG	GATGGTAGAT	GATTTGGAAA	AGGAAATCC	3600
AAGGATTTTT	GATGATCCAT	CTAAGACTTT	TATTGATTTA	TATATGAAGT	CAGGCCCTCTA	3660
TATTGCAGAA	CTTGGAAGC	GTTTATATAA	TAGCAATGGC	TTGAAAGAGG	CCTTTCCAAA	3720
TCCTGAAGAA	CGCTTAJAJC	ATATTTTGGG	AAAGCAAGTT	TATGGATTGG	CTCCGTCTGA	3780
GATTATCTAT	AACATTTCCA	CTAATTTTAT	ATTTGGCAAT	CTTTCTAAAG	ATATCAGTAG	3840
GAAGAATTTT	GTTTTAGCAG	ATACCATTC	AGCGCTAAA	GAAGGGAGCA	TTCAAAAAGTT	3900
GGTGTATTCC	TATTTTGAAA	ATAATTAAAA	AGAAGGCGGA	GTCAAAATTC	TTTGAAATCA	3960
GAAAAAACGC	ATAATATTGA	GTGCTTTTGT	ACTGCCCCCC	AAAAGTTAGA	CAGAAAAAAT	4020
CTAAGTTTTG	GGGGGCAGTT	CAGACAATCC	TGTGATTATT	GCGTTTTATT	GTGGGAAGAT	4080
GTATAATGGA	TTGAAATAAG	ATATGAACAA	ATCAATTAGG	AATTTAAAGC	ATTTTNTAAT	4140
AACGTTTTAG	AGTAATGGGG	GGCTATTCCA	ACTTCAACCT	ACTATAATAC	AGAAAAAAAC	4200
AACCTCCCTGA	TAATTCAGAG	AGTTGTCTAT	AGTTAAATTA	GTTTTTAGAA	GCTTCTTGGA	4260
ATTTCTGGGT	TTTCCATGCT	TGCTCAATGA	TAGCTTGTA	TTCTTTAGCA	GATGCTTGCA	4320
TTTTTTGAGT	TTCTGGCTCG	TTCAATGGGA	TATTACTG	ACGAACGATA	CCATGTGCAC	4380
CAACAACAGC	TGTTTGACCG	ATAAAGACAT	TCTCAACTCC	GTATTGACCT	TCTTGGATA	4440
CTGAAAGTGG	AAAGTATGCG	TTTTCATCGT	CAAGAGTTGC	TTTAGTGATA	CGAGCAAGGG	4500
CTACTGCGAT	ACCGTAGTAT	GTTCACCTT	TTTTGTTGAT	GATTTGTGAT	GCTGCATCAC	4560
GAACACCTTC	GAACAAATCA	ATCAATTTCAG	CTTCTTGAAC	ATTTTGAGTG	TCTTTAAGGA	4620

1246

ATTCTTCAAG GTTACACCA GCGATGTTAG CGTGTGACCA AACAGCGAAC TCAGAGTCAC	4680
CGTGTTCAAC CATGATGTAG GCGTGCACTG AACGAGCATC CACATCCAAT TTTCAGCAA	4740
GTGCTTGACG GAAAGAGCT GAGTCAAGTG AAGTACCTGA ACCGATAACG CGTCTTTAG	4800
GGAAACAGA GAAATTCCTA GTTGAGTAAG TCAAAACGTC AACTGGGTTA GCAGCAACAA	4860
GGAAGATACC TTGAAACCA GATTCAACAA CTTGAGTTAC GATTGATTG TTGATAGCAA	4920
GGTTTTTACC TACAAGTCA AGACGAGTTT CACCTGGTTT TTGAGGTGCA CCGCAAGTGA	4980
TCACAAAGG GTCAGGCTC GCACAGTCAG AGTATTGAGC TGCATAGATT TTTTAGGGT	5040
AAGTGAAGC AAGGCGCTGA CTAAGGTCAA GCGCATCACC AACAGCTTTT TCATGCAATT	5100
GTGGAATTC GATAATTCCA AGCTCTGTG CAATTCCTTG GTTAACAAGT GCAAAAGCGT	5160
AAGATGAACC TACAGCACA TCACCGACAA GGATAACTTT TTCTGTCTT TTAGTTGAAG	5220
TCATTGTTTT AAACATCTCC TTAATTTTAT TAGGGGATTT TCCCTAGACA ACTTCATT	5278

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

ATAAGGAATC TCTAAAAAT TTAAAGGAGA ATCTAGACAA TGGATTTCAC ATGGGCACTG	60
AAGTATGCCA CTGAATTTT GGGAACTGCC ATTTTGATCA TTCTTGGGAA TGGTGCAATT	120
GCCAACGTTG AACTTAAAGG TACGAAAGGT CACCAAAAGT GCTGGATCGT CATGCTGTGT	180
GTTTATGGTA TGGGGGTTAT GATCCCAAGC TTGATGTTTG GTAACGTATC TGGGAATCAC	240
ATCAACCTGT CTTTCACCTC AGGGCTTGCA GTTAGCGGTC TTTTCCCTTG GGCACAAGTG	300
GTACCTTACA TTATCGCGCA AGTCTTGGGG GCTATCTTTG GCCAAGCCTT AGTTGTGGCA	360
ACATACCGTC CATCTACTCT GAAACTGAA AACCACAAAT ACATCTTGGG AACTTCTCA	420
ACTATTTCAA GTATTGACCA TGGTACAAA GAAAGTCGCT ATGCAGCAAC TGTCAATGGT	480
TTGATTAAAG AGTTTGTGG TTCAATTTGT TTGTTCTTTG CAGCTCTTGG TTGACTTAAA	540
AACCTTCTTG GTGCTGAAGT GCTTCAATTC ATGAAACAAA AGGCACAGA AGCAGGACAA	600
ACAGTTGATT TTTCTGACTT GGCTATTAAA GCACAGGTGG CTCCACACAC TGCTTCAAGG	660
CTTTCTGTGG CTCACITGGC ACTTGGATTC CTGCTTATGG TTTGGTAAAC ATCACTTGGG	720
GGACCTACAG GACCTGCCCT GAACCCAGCC CGTGACTTGG GACCACGTCT CCTTCATGCT	780

1247

TTCCTCCCA AATCAGTCTT TGGTGAGCAT AAAGGCGATT CAAAATGGTG GTATCTCTGG	840
GTACCAGTAG TAGCACCTAT CGCAGCAGCA ATTGCGGCAG TAGCTGTATT CMAATCCTT	900
TATCTCTAAG AANTAGCTCC TTAAACATTT GAGTGAGCAC CATCTATAAG TAAGAGAGGA	960
TCAGACTGSK TCTCTCTTTT kGATTTTtG GGAATGAAA GAACTCTAAA CAACTCCTC	1020
TCCAGCAOTG GTTTAGAAGT CTCAGTGGGC TATTCCAGCT TCAATGGACT ATAGTAGGTT	1080
GCAGTTGAAA TAATAGACCC TTGTTTCTAA AACATTGTGA GAAATTGGTT TGAATTCCTC	1140
AATCAAAATG TGCAGTTTTC ATTCTACTAT ATATTATCG AATATTATCG GAGATGGGTT	1200
CCCTATCTTG TAAGTCTGCT TTATAGTGGG TTGAAGTGG AATAGTCCCT CCTTCTTCT	1260
CAACATTTGT GAGGAATGA TTACCTTCC TCAACAAAAT GTTCAGTTTC TATTTCATTT	1320
TACTATAAAA TANGOGATTA GGGGGGCTAT TCTTGCACCT ACATTGACTC TGCTGAGTCC	1380
TATGATTTGT ATCGTTTAT CTGCAATTTT ATACTCAATG AAAATCAAG GCAAACTAA	1440
GAAGCTAGCC GCAGGTGTGT CAAAACACAG TTTTGAGGTT GTATAGTAGA TTGAACCTAG	1500
AATAGTACAC ATCTACTTCT AAAACATTGT TAGAAATCGA TTTGACTGTC CTGAACGATT	1560
TGCCCTATTC TGTGTTTATT TTACTATATA AACCAGAGAC TGTTTACATT TTCAGCAAGT	1620
GAGTGATGG ATAAATGCTGA AAATCCTTG AAGGATAAGT CTATTTAGTA CTTTCTATTA	1680
ATTAGTTAAA TTTTACCAA GAATAATTCA CAAAAACGTT GTAAAAACAT TGCAATTTAG	1740
CTGAATTTG ATAAAAAGT AAGGAAGTT AGACTGTATT GCCTACTGTC TATCTATAAA	1800
ATATATTTTA TTGGAGGCTT TTACTCAAAAT GGCAAAAGAA AAATACGATC GTAGTAAACC	1860
ACACGTTAAC ATTGGTACTA TCGACACGT TGACCACGT AAAACTACCC TAACTGCACG	1920
TATCACAACG GTTTTGGCAC G	1941

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATTTTGAAGAA ATTGAAGAAA TCGTAGCCCC TACAGATGGT GAATTTTGG GGGAGGTTT	60
ACTTGAACT GGGGTAGTTC TCTTAATTGG AGTAGCCTGT TGTAAAAAG ATAGGGAGTG	120
ATAATCATGC AAGATAACTT TTTATTGAG GAAATTGAG AAATTCAGT ACCAGTTAAT	180

1248

GATTTTTCAG CTGGAAGTGC AACAGGTATC GGATTGGTT TAGCAATCCT TGCTCTTGCT	240
GGTTGTTCAA GTTGTTCAT TTAATAACAT CAAGCTTTT CAATTTTATT TTAGACAGTC	300
ATTTAAATTT TCCGTATTAG TCTTGCAGCA AGAGATTAAT AGAATTAGTC ATTATTTTAT	360
TCATTGCGGA CTGAGGGACT AGAGTATGTT TTACTTAACC CCTCTTTTAT TTATTAAAGG	420
TTAGCTTTGT TATGAGAAT GTTGATAAGA TTAAGATATT ACCTACTCCT TATGAGGGAC	480
ACTATCATT ATATATACCA TCCAGTAAGA AACATGATT AGTTGGGAAA CAGGAAAAAA	540
ATGGTTAGAG CAACATAAG GTCAAGAAAT TACCATATCG GACTTATTAG TGTAGTAGG	600
GAAGAAATAT TTTTAAATA TCTTGGGACT TTAATATAAC ATTATCTGAA AATTAAACT	660
ATAAAGATT TAATAAGAAT TTTGAAAAAA TCCTATCTTG TTGTCAATT ATTTGCAACG	720
ATACATGAAA TTAGTCATGC AATAATTGCT AATAA	755

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CCAGAAAAAC CGTAGTGGAG CTCGTGGAAC AGTGAATTG ATTTTCCAAA AAGAANTACAA	60
TAAATTTTCA AGTATCTCAA AGAGGGAGGC ATAGATGTC AGATGCATT ACAGATCTAG	120
CCAGATGAAA AAAAATCAAA GAAGAAATCA AGGCACATGA GGGACAAGTC GTAGAAATGA	180
CTTTGGAGAA TGGTCGTAAG CGCCAAAAAA ATAGATTGGG TAAGCTAATT GAAGTTTATC	240
CACCTCTATT TATTGTGGAG TTTGGGGATG TGAAGGAGA TAAACAAGTT AATGTTTACG	300
TTGAATCCTT TACTTACTCA GATATTCTTA CAGAAAAGAA TTTGATTAT TATCTTGACT	360
AAAGTAGAAA ATTTTCTCAC TTTTCTTTT TTCTCCGAAT AATTTAGGTG AAGGCAATCA	420
TCGCTTTATA TTATTTTTC AGGAGGAAGA ATGAAAAATT TACCGTTTAT AGCAAGAGGA	480
ACAAGTTATT ACTTGAAGAT GTCAGTTAAA AAGCTTGTTC CTTTTTAGT AGTAGGATTG	540
ATTGCTAGCAG CTGGTAGATG TGTCTATGCC TATCCAGAG GAAATGGATC GATTGCGCT	600
GGGGATGATT ATCCTGCTTA TTATAAAAAA GGGAGCCAGG AGATTGATCA GTGGCGCATG	660
TATTTCTGTC AGTGACTTC TTTGTAGCC TTTGTTTGA GTAATGTCAA TGGTTTGTAA	720
ATTCCGGCAG CTTATGAAA TGCGAATGAA TGGGACATC GTGCTCGTCG GGAAGGTAT	780
CGGTAGATA ATACACGAC GATTGCTTC ATTACTGGT CTACTGCAGG AACTTATGCT	840

1249

CATGTTGCCT GGGTGTCAAA TGTAATGGGA GATCAGATTG AGATTGAGGA ATATAACTAT	900
GTTTATACAG AATCCTATAA TAAACGAGTT ATAAAGCAA ACACGATGAC AGGATTATTT	960
CATTTTAAAG ATTGGATGG TGGCAGTGT GGAATAGTC AATCCTCAAC TTCAACAGGC	1020
GGAACTATT ATTTTAAGAC CAAGTCTGCT ATTAAACTG AACTCTTACG TAGCGAACT	1080
GTGATTGATT ACTATTATCC TGGGAGAAG GTTCATTATG ATCAGATACT TGA AAAAGAC	1140
GCCATAAAGT GGTGAGTTA TACTGCCTAT AATGGAAGCT ATCGTTATGT TCATTGGAG	1200
GCTGTGAATA AAAATCCTCT AGGTAATCT GTTCTTTCTT CAACAGGTGG AACTATTAT	1260
TTTAAGACCA AGTCTGCTAT CAAAACGTAA CCCCTAGTTA GTGCAACTGT GATTGATTAC	1320
TATTATCCTG GAGAGAAGT TCATTATGAT CAAATTTCTG AAAAAGACGG CTACAAGTGG	1380
TTGAGTTATA CGGCTTATAA CGGAAGTCGT CGCTATATAC AACTAGAGGG AGTGACTTCT	1440
TCACAAATTT ATCAGAACTA ATCAGGAAC ATCTCTAGCT ATG	1483

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1027 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CCCGGAAAC AAGTTAAAGT TGAAGTTGGT CAGCAGTTT ACGTGAAAA ATTGAACGTT	60
GAAGCTGCTC AAGAAGTTAC TTTTAACGAA TTGTTCTTGT TGGTGGTGA AACACTGTTG	120
TCGGAATCC ACTTGTGCT GGAGCTACTG TAGTTGGAAC TGTGAAAAA CAAGGAAAA	180
AAAAAAGT GGTACTTAC AAGTACAAAC CTA AAAAAGG TAGCCACGT AAACAGGTC	240
ACCGTCAACC ATATACAAA GTTGTCTCA ACGCAATCAA CGCTTAATT TANGGAGAAC	300
ACATGATACA GGAGTCTTT GAGAGAGCCG AAGATGCCA GCTGAGGAGT GCGGAAATTA	360
CTGACACGC CGAGAGTGGC GAATACGGCT TAGATGTCGT GTTGCATCG GTTCTACGC	420
TTGCCATTAA CTTTATCAAT TCTATTGAGA AATTGACAG CTATGAACCA ATCTAGAAAT	480
TAAACGAAGA TGAAGGTGGC TATCTGATGG TTGAAATACC AAAAGATCTT CCTTCACACC	540
AGAGAGAAAT GACCCAGTTA TCTTTTGAAT CATTTCCTT AGGTATGGCA AACTTATCGG	600
ACAACATTTC TGAGTTCGTC CAAACAGAG TTATCAGCA AAACATAAC GGAGGAAAA	660
ATTATGTAA AAATGACTCT TAACAACTTG CAACTTTTCG CCCACAAAA AGTGGGAGGT	720

1250

TCTACATCAA ACGGACGTGA TTCACAAGCA AAACGCTTGG GAGCTAAAGC AGCTGACGGA	780
CAAACTGTAA CAGGTGGATC AATCCTTTAC CGTCAACGTG GTACACACAT CTATCCAGGT	840
GTAALACGTT GTCTGGTGG AGATGATACT TTGTTGCTA AAGTGAAGG CGTAGTACGC	900
TTTGAACGTA AAGGACGCGA TAAAAACAA GTGTCTGTTT ACCCAATCGC TAAATAAAAA	960
GGTCCATGTA ACCTTTTATC CCGAACCTTG AATGTAGAG GTAGGGAAGC TAGAAACAGC	1020
TTAAAAAT	1027

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1990 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CGGTTCAJAT GTGTCAGGTA AATCTACGTT AATTAATTCT ATTGTAGGTT TTCAAGAGAT	60
TTATTTAGGA GAAATAGAGT ATTGTGATAA AGATTTGATA GTTAGTTCTC AACCTTTTGC	120
TCATTTAGGC TTACTCCTC AAACACAGT AATTCATTTT TATACTACTG TGAAGGACAA	180
TGTAATATTG GGGCTGAACC TTGCTGGAAA GTTTGGGAAA AATGCTGAGA ACTTGTGTCA	240
AATAGCCTTA GAAATTGTTG GGTAGCTGA TAAAAAAAAT AATTGTGTAG AACATTGTC	300
AGGTGGACAA CTGCAACGGT TCCAGATTGC TAGAGCAATA GCTCATAATC CAGATTTTGA	360
TATTTTAGCA GAACCTACCG TTGGTTTAGA TACTGAATCT GCCGAAAAAT TTTTAATGTA	420
TTTAAAAGAT AAGAGTTTGG AAGGAAAAAC TATTATCATA TCTTCACATG ACATAAATCT	480
ACTCGAAAAA TTTTGTAAAA AAATACTTTT TTTACAAAAT GGCTCCATAT CATTTTTTGG	540
TGATATGCGT GACTTTGTAG ATAATTCAAC TATCAAATTA AATTTTTCAT TGCAGATAG	600
AATTTCTAGA TATCAAATTG AATTTTLAGA AATTTTLAGA TTTAAAGTTC ACATCGAAGA	660
TAATGATAGT TTTCAATAG AAGTCCCTAT AGAAGAAAAG ATCTTAGATG TTATCAATGA	720
GGTAGGAAAA GCATGTGAAA TFAAAAACCT TTCAACAAAT AATTTAACCT TACAAGAAAG	780
TTATTGTCAA AGAATAGGAG GAGAAAAAAT AAGGCTGATC AATTAAAGCA CAAATCGAC	840
TIAGGTTTAA GAGGTCTAGC GATTATTGCT AAAAATGAGA TTATTGCTTT TTTTAGAAT	900
AAAGGTTTAA TTATTCTTCA GTTTCTACAA CCAATCTTAT ATGTTGTTTT TATAATAATA	960
GGATTAAATT CTTGATAAAA GAACATTGAG TTTAATGATA TAAAAACCTC TTATGCGAAG	1020
TATACAATCA TTGGTGTTAT AGCTTTATTG ATAAATCGGC AGATGACTCA AGTATTATTAT	1080

1251

AGGGTGACAA TAGATAAAAA ATATGGGCTA CTGCTCTTA AGTTATGCAG TGGAGTCTGT 1140
 CCTTTATATT ATATTTTAGG GATGAGTATC TATCTATAT TAGGGTTGAT AGTTCAAGAA 1200
 ATTATTATNT ATATAATTAC GTTAGCGTTT GAGATAAATA TCGCAATGGA TAGATTTTTT 1260
 TATACAGTTT TGTATCTAT TGTGTCTTA TTATTTTGGG ACTCCCTTGC AATTTTACTT 1320
 ACAATGTTTA TCAATGATTA CAGAAGACGT GATATTGTAA TACGTTTTGT ACTAACACCG 1380
 CTGCGTTTTA CAGCTCCTGT TTCTACTTA ATAGATTCTG CTCTAGTAT TGTGAGATGG 1440
 ATTGGTCAGT TAAATCCCTT AACTTATCAA TTAATATTT TGAGAAACTT TTATTTTAAA 1500
 AATTCACAA CTTTGGAATT AGTTTTCTTA TTGTTAACAT CATTACTTGT CCTTATATCT 1560
 GTATCTTTTA TTATACAAA GATAAAATTG ATACTGATAG AAAGATAAAA GTTGGGTCAT 1620
 CCAACTTTTT TGTGTCTCC CGAAAACCA TAGCTATGCT AGTGGTTCCA TAGAGCTTTT 1680
 AGCGTGGTAA CAAAAGAAC CTCCTAAAT GATAGATAG AAGTGGTTTC TCCGCCACTA 1740
 CAACATATCA TACAGGAGGT ACCTCATGAG AGAGGATAAT CAAAGTTTAT CACATACCAC 1800
 ATGGAATTGT AAATATCATA TTGTTTTTGC ACCCAATAT CGTCTCAA TCATTTATGG 1860
 CAGATACAAA GCTAGTATCG GAAGAATCAT ACGTGACTTA TGTGAGGTA AGGGTGTAAT 1920
 AATCCATGAA CGGAATGCTT GTTCAGACCA TATTCACATG CTTATCAGTA TTCCTCCGAA 1980
 ACTTAGTGT 1990

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GAACATATTT GCATATATTT CTAGCAATGA TCATGGCGAA TCTTGGTCTG CACCAACTTT 60
 ATTACCTCCT ATAATGGGAC TTAATCGGAA TGCCCATAT TTAGTCTCTG GACGTGGAAT 120
 CATTGAAAGC TCAACTGGAC GTATCTTAT TCCGCTTAC ACTGTAAAG AGTCTGCGTT 180
 CATTTATAGT GACGATAATG GAGCATCTTG GAAAGTTAAA GTAGTGCCAC TTCCTCTAG 240
 TTGTCACGCA GAGCAACAAT TTGTAGAATT GAGTCCAGGA GTAAATCAAG CATATATGCG 300
 TACAAATAAT GTTAAATTTG CATATTTAAC AAGTAAAGAC GCAGGTACTA CTTGAGTGC 360
 ACCGGAATAT TTGAAATTTG TTTCAAATCC AAGTTATGGA ACACAAATAT CAATCATCAA 420

1252

TTATAGCCAA TTGATTGATG GTAAAAAGGC TGTCATTFFA AGTACTCCAA ACTCCACAAA	480
TGTCGTGAAA CACGGACAAA TTTCGATTGG TCTAATTAAAT GATGATAATA CAATTGATTG	540
GCCTTATCAT CACGAOGTTG ATTATAGTAA CTATGGATAC TCATATTCAA CATTGACAGA	600
GTTACCAAAAT CATGAAATTTG GATTGATGTT TGA AAAAATTT GATTTCATGGT CTCGTAATGA	660
ACTTCATATG AAAAAATGTT TACCATATAT AACATTTAAG ATTGAAGATC TGA AAAAGAA	720
TTAAAGCTGA AATTTGAAAA TATATAAAAA GAGGATAAAA ATTATGTTAA ATTACGGTAT	780
TGTTGGAGCT GGATAATTTTG GAGCTGATTT AGCTCGCTCA ATGAACAAAA TTGAAGATGC	840
AAAAGTGGTT GCGGTATTTTG ACCCAAATCA TGGAGAAGAA GTTGCTCAAG AGTTGGGATC	900
AGATGTTTGT GCAAGTTTAG ATGAACCTGT AGCACGTGAA GATATTGATT GTGTGATCGT	960
AGCTTCACCT AGCTACCTTC ACCGTGAACC AGTGTGAAA GCTGCTCAAC ATGGCAAAAC	1020
CGTATTTTGT GAAAAGCCAA TTGCATTGTC TTATGAAGAT TGTAAAGCCA TGGTTGACGC	1080
ATGTAAAGAA AATAATGTCA TCTTTATGGC TGGTCACATC ATGAACCTCT TTAACGCTGT	1140
ACACCATGCT AAGGAATTTGA TTACTCAAGG TAAAAATCGT AAAGTTCTTT ATTGCCATGC	1200
TGCTCGTACA GGTTCGGGAG AACACAACCC AACTGTATCA TGGAGAAGAA TTCGTCTCTA	1260
ATCTGGAGGA CATTTGTACC ACCAATATCA TGAATTAGAT TGCATTCACT TTATCATGGG	1320
AGGACTTCTT GAAAAGCGA CAATGGTAGG AGGCAATGTA TATCATTAAG GTGAAAACCT	1380
TGCTGATGAA GATGATATGC TCAATGTAAA CTTAGAATAC TCTGTGATC GTTATGCTGT	1440
TTTGGAAATAT GGTAAATGCTT TCCGTTGGGG TGAACACTAC GTCTTGATTC AAGGAACATG	1500
AGGAGCTATC AAATCTGACT TGTTCAAATC TGGCGGTACT CTTCGTGTTA AAGGTGAAGG	1560
AGAAATCACAC TTCTTAGTTC ATGAAATCTA AGAGGAAGAT GATGATCGTA CAGCTATCTA	1620
TACCGGTCGT GGTATGGATG GAGCAATTGC GTACGGTAAA CCAGGAGTAC GTTGCCCAT	1680
ATGTTTCCAA ACATGTATTG ATAAAGAAAT GGAATATCTA CATGACATCA TTAAGCTGG	1740
AGAAATTTACA GAAGAATTTG AAAAACTTCT CAATGGGTGA GCTGCTTAG AATCAATGCC	1800
TACCGCTGAT GCATGTAATT TATCAGTTAA AGAAGATCGA AAAGTAAGTC TTTCAGAAAT	1860
CACAAATGCT TAACTTTGT AAAACAGAAT AGTAATTTCT TGTCATTAATA TAATTTCTAA	1920
AGTTCTGTGA TACAACCTAT TGAATAAAGA AATAGAGATG GGACTGGGAT AATGCCCATG	1980
CCCATTTTTT ATCAAAAAGT AATGAGATCA AAAATGTGGC AGTGTGAAA TGAAGATTTA	2040
AGGTATCGAT ATTGGCGGAA CAACAAATTA GGCAGATTTA TACGATGAGT TTGGAACGAG	2100
TTTGAATCAT TTCAAGGAGA TAGAAACAAT TATTGACTAT GATTTCGGAA CGAATCAGAT	2160
ATTAAATCAG GTCTGTGATT TAAATGGTGA GTATACTTTA AATCATTCAA TTGATGGTGT	2220

1253

TGGGATTTCC	ACTGCTGGAG	TGTTAATGC	TAATACTGGA	GAAATCATCT	ATGCAGGCTA	2280
TACAAATACCA	GGGTATATCG	GAGTAAACTT	TACTGCCGAA	ATAGAAAAAC	GTTTTGGGT	2340
GTATACTTTT	GTGAAAAATG	ATGTTAATTG	TGCTGCATT	GGTGAATTGT	GGAAGGGACA	2400
AGCCAAAGAT	ANGAAAAATG	TAGTAATGGT	TACTATTGGA	ACAGGTATAG	GAGGCGGTAT	2460
TATTGTCAAC	GGACAAATG	TTAACGGATT	TAACATACT	GCTGTGAAG	TAGGTTATAT	2520
TCCTGTAGGT	AATTCGGATT	GGCAAAGTAA	AGCCTCAACA	ACCGCATTGA	TTCATTATATA	2580
TCAAAAAAG	AGCTTAAAA	CTAATCAAA	TGAGCGTACT	TTCTTCACTG	ATTTAAGATC	2640
TGGAGATAAA	GTGCTGAAG	AAACTTTTGA	AATTTTGTGA	GAAATCTAA	CAAAAGGTTT	2700
ATTAAACGATT	TCTTATCTAC	TEAATCCAGA	AATTCCTATA	TTAGGAGGTG	GGATTCTGGA	2760
TAGTAAGGAT	ATTTTGTTC	CTGAAATCA	AAGTCTTTA	GCTAAAAATG	CAATGGATAA	2820
TAGGTTTTTA	CTTAAAAATC	TTGTGGCAGC	TACATTAGGA	AATGAAGCTG	GTCTATAGG	2880
AGCTGTAAAA	AATTTCTTAG	ATGAAATTTT	TAATAAATAG	TATGTAAAGT	AAGGAGGTGT	2940
CACAATGACT	AACCTCTGAT	TTTCGACAAT	GCAAGATATT	GAGAATGTG	CAACGATAT	3000
TATAAAATCA	TATGATAATG	AGATTTATAC	TTATAAGCT	GTTTCCCAAG	ANGAATGGAA	3060
AAAACCTAGAA	AAAAGTTATG	ATGAAAAAAG	TCACGAGAA	TTAGTTTCAA	TAGAAAGCAA	3120
TTTAGAAAA	GAACAAACAG	ACCTTATTGA	TGAGGTTAAT	AAAACAATCA	AGGAAAAATGA	3180
TGCAAAATATT	CAGTATATTT	CATCAAGTAG	GAGAGGAGAA	TTTGTAGAAA	AAATTATTGG	3240
TAGGGTGGTA	GAAAAATATG	GCCATTAGTC	AGATGAAAA	AATCTCTCTA	CTATTTTCTA	3300
AAAGTAGTCT	TGATGATGTT	TTAAAACTA	TTCAAGAACT	AGAGTCAGTG	CAGTTCGCTG	3360
ATTTAAAGGT	TCAGGATAAC	TGCTCAGAAG	CTCTAGAAAA	AGATGAAGTT	GTATTTCCAA	3420
CTATTCAAA	TTTTCTACT	TCTAATTTCA	ATCATGGGGT	TATTGAGGGA	AATGATGCCT	3480
TGACTTATTT	GATGAATCAA	CAACCAACAT	TAGAGCAAC	TGTAGAGAAA	TTACAAGAAT	3540
ACCTACCGAA	AGAAAAACAG	TTTAATTTAT	TGCAGCAACC	TCCGATAACT	ACCTCTTAGT	3600
AAGAATTAGA	GAAATTTGGT	AAAGCTAATG	TTGCTGAGGG	TGTTCTTAAA	AAAGTGAATC	3660
ATCAAAATTA	CAGAGTTCA	GAATTAGAAA	GACACATTCA	AAGTAATAAT	GAGGAAATAG	3720
AGCGATTAA	AAAGTGGGAA	AAATTAGAAA	TTGTCTCTCG	GAAATTAGAA	CAATTTTCTT	3780
TCTGTAAAGG	AAAAGTCGGA	ACAATTTCAA	GGACTGAAGA	TAATCGCTTA	TACAAATAGTC	3840
TTTTAGAAAA	CAATATTGAA	GTCAAGAAA	TATTTTCTAA	TGATAGAGAG	TACGCTGTTG	3900
TGTGTTTCTA	TCAGTCTAGT	TACTCTATAG	ATTTTGATGA	ATACTTATTT	GAACCATTTG	3960

1254

ATTATTCTAG AAAGGAAMTA CCGAAGCAGC GAGTAGTAGA TTAGATCAA GAAAACATGC	4020
AGTTAATAAC TGAAAAAGAG AATATTATCG CATCGTTGCA AGATTCAAAG AAATATTTGA	4080
TAGATTTACA ATGGCAAATA GACTATATTT TATCTATCTA TGCTGCTCAA ATCTCTAAGA	4140
ATAACTTTTT GTGCACCTCG CATCTAGTTG CATTAGAAGG ATGGATAGAA GAAACTCGTA	4200
TTTTATFATT TATAAAAGTT ATGGATGAGC ATTTTGGACA TTCTATTAT ATTTATGAAT	4260
CGGAACATT GACGATAAT CAAGATGAAA TACCTATCAA ATTAACGAAT CATTCCTTAA	4320
TTGAACCAT TGAATTATTG ACAGAAATGT ATGCTCTGCC CAAATATTTAT GAGAAAGATC	4380
CTACACCTGT ATTAGCACCA TTTTACTTTA CATTTPTTGG AATGATGOTT GCTGATTTAG	4440
GCTATGTTTT ACTATTGTTT TTAGGAACAA TGTTAGCATT AAAAATTTTT CATCTACCTT	4500
CAGCAACTAA GAGATTTTTA AAATCTTTA ATATATTAGG GGTAGCCGTT GCAATTTGGG	4560
TGGGAATCTA TGGCTCATTT TTTGGATATG AGTTGCCATT TCATCTGATA TCTACAACCT	4620
CTGATGTGAT GACTATATTA TTAGTGTCAG TTGTGTTTGG GTTATTACA GTATTGACAG	4680
GTTTGTTAGC TTCAAGACTA CAAAAGTAA GAATGAATAA ATATGCAGAA GCATATAATT	4740
CAGGATTGCG GTGGTGTGTT ATCTCG	4766

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

CCTTTTAGAA AAAATTAAAG AATACGACAC CATTATCATT CMTCTCAT TGA AACAGA	50
CCCTGATGCC TTGGGAATG AGTGGGATT GAAAGCCTTG CTGGAACATC ATTTCCAGA	120
AAAAACCATC AAAGCGTCG GTTTTGATGA ACCAECTCTT ACTGGATGG CTGAGATGGA	180
TCTTGTTGAA GATAGAGCCT ACCAAGGCGC ACTTGTATC GTCTGTGATA CAGCTAATAC	240
TGCTCGATC GATGATAAGC GCTATAGTCA AGGTGATTT CTCATTAAAG TTGACCACCA	300
TCCAAATGAT GATGATACG GTGACCTGTC TTGGGTCGAT ACTAGTCAA GTAGCCGTAG	360
aGaTGATTAC CCTATTTGCC CAAACAACCC AACTAGCCTT GGCAGATCG GATGCTGAGT	420
TGCTCTTTGC AGGAATGTC GGTGATACAG GTGCTTCTCT CTACCTTCTT ACCACTGCAC	480
GGACTCTTGC CCTGGCTGCT TATTTGAGAG AACATAACTT TGACTTTGCG GCTCTCACTC	540
GC AAAATGGA CACTATGAGC TACAAAATG CTAACATGCA AGGCTACATC TACGACCATC	600

1255

TGGAAGTGGG	TGAAAATGTT	GCTGCTCGCG	TTATCCTGAG	TCAGAAAATC	TTGAAACAAT	660
ACAATATAAC	CGATGCTGAA	ACTGCGGCCA	TTGTAGGTGC	ACCTGGACGC	ATTGACAGAG	720
TGAGTCTCTG	GGGAATTTTT	GTCGAACAGG	CTGATGGCCA	CTACCGAGTT	CGCTTACGCA	780
GTAAGTCCCA	TCCATCAAT	GAAATTGCCA	AGGAGCATGA	TGCTGGAGGC	CACCTCTAG	840
CAGTGTGTGC	TAATTCCTAT	AGCCTAGAAG	AAAACGAAAT	CATCTACCAA	AAGTTAGAAG	900
ACTTGCTTAA	AAACTGATAA	AATACTTGCC	AAACTTTTCA	GAATCTGATA	GACTAGTATA	960
GTAACAATCT	ATGGCTCGCA	AAGAGACCAT	GGCAGAAAGG	AAATATTGCA	AAATGAAAAA	1020
AGATATCCAT	CCAGAAATATC	GCCAGTTGT	CITCATGGAC	ACAACACTGT	GTTACCAATT	1080
CCTTAGCGGT	TCAACAAAAC	GCTCTAACGA	AACAGTTGAG	TTGGAAGGCG	AAACTTACCC	1140
ATTGATCCGT	GTGGAJATTT	CATCAGACTC	ACACCCATTC	TACACTGGAC	GTCAAAAGTT	1200
CACCTAAGCA	GATGGACGGG	TGGATCGTTT	CAACAAAAAA	TACGGTCTCA	AAATATGATA	1260
AGAGAACAGT	TTTGCTGTGT	CTTTTTGTGT	TCTTGAATTC	AACGTCTGTT	TTCAATGTTCC	1320
AGACTCATCT	GTAGGTTGGA	TTTCCATGCT	ACTAGGCAGG	AAGGAAATAG	CTGTTTCAAC	1380
ACGTCCTATA	TGAGCTATAC	TATTTGTGAG	AACCACACTT	TCATTTGATG	TCCAAGTGGG	1440
ATTCAITTTT	TTAAAAGCTT	CTCGGACTTT	TTCCAAATCT	TTGGAGGCCA	TGGCTGCTTC	1500
TAAGGTTTCA	AAACGAGGAC	TATATCTCAT	CTGCTTTCAA	AAAGCATTCCT	AGTCCATCTC	1560
CGATTACCGA	TGGACTTTAT	CACCTCCTTC	TCCAGTCTTT	GTATGACATC	TTGAAGTTGA	1620
TTTATGACAT	CTTCCAAAGT	TCGAAAAGCT	TTATTTCTAA	ATCCACGTTT	ACGAATCTCT	1680
TTCCACACTT	GTTCAAATGG	TTTATCTCTG	GTGTGTATGG	AGGAATAAAG	GTAAAATCAA	1740
TATTAGTGGG	AAATATTTAAG	GTACTTTGAT	TATGCCATAT	AGCATTTGTC	ATAACAGGTA	1800
AAAGGATAAG	CTTTGGAAG	CTCTTCTAAA	AAGCGTTTCA	TCCACACTCC	TTTTTATAAA	1860
CTTGAAATAA	GGCATCAATT	GTAACAAATT	CTCCTGCCTC	TGTAGCCTTC	AAATGACGGG	1920
CAAGAAAGGC	TTTCTCTTCC	TCAACTGTCA	TATATGCATG	GTTACGACCA	CCACGTGTTT	1980
CTTGAAAGGAG	AGAGTCGAGT	CCGAACCTCT	CATATTTTTT	TACGTTTTCG	CAATGCTTTG	2040
TTTGATTACA	GTCTAAAAGC	TCTATAATCT	CTTTATTAAGA	TTTGCCCATC	AGACGAAATA	2100
TAGTAGATTG	AAACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTGTTAG	AAATCGATTT	2160
GTCTGTCTCT	TGTTTCACTT	TACTATAGAA	CGATTTGAAG	GCGTTTATAA	TATTTAGCTG	2220
TACGAGAGTC	TTTTAAAAGT	GTTTGTATGG	TTTGGATTTC	TTCTTTAGTT	GATTTCATAT	2280
TACTATTATA	TAAATGCTTTT	TGATTTTAGT	CTGGTATAAA	TATTTGCTTC	CTCCAAAAATG	2340

1256

GTCAATAGTTT TACTGSCAAA TCTAACATAT CACGATATAA TTAACAAGTG ATTTCTGAAT	2400
TGCTAAACAT TTCTTTTCT TATAGCATAC TTAAAGATTT TGTCTTTGAG AAAGATATTT	2460
CCAAGAAAAA OGTTGTTTTT TTGG	2484

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CTAGATATAG CTATAATTTT ATTTATAACA AGAGGATAGA AATGACCGAA TTAGAAAAGAA	60
AAAATCGAAA AATTAGCTAA GAAATATTTCT GATAACTTAA ACATCAAAGT TCAAGAGAGA	120
GTTCCTGAAA TGGCAATGA TAAATAGAGC CATTAATTTGA TATACAGAGT TTTAGGTAT	180
TCMTTGAAG AAGGAGAAAA TATCGATTGT TATCAAAATA AAGCTCGTTT TTTATACAAA	240
TATGCTGGTT CATTTTGTAGA AGAAGCTGCA GFACTATGCT TTAACGAAAA ATTTGGTACA	300
GAAAAACCTT AAAAAGTTAA CATTCCTAAT TCTGAAAGTA CAAAACCTAA GACTTTTGAA	360
ATTGATTGTT TAGTCGGAGA AAAACACGCA TACGAAATAA AATGGTGGGA TGCAACTACA	420
GATGGAGACC ATATAACTAA AGAACACACT AGAATAAAG TTATTCATAA CAAAGGATAT	480
ATACCAATTC GGTAAATGTT CTAATATCCA AATGAACTC AAGCTATAAA AATTACAGAA	540
ACTTTAGAAA CATTGTATAA OGGTATTGGA GGGAAATATT ATTTATGGGA TTCTGCGCTGG	600
GAACATTTAA GAGCAGTGAC CGGTATTGAT TTACTTAGTA TTCTAACAGA TATTGCAAA	660
AAAAAAACAG GGCTAAATC AAAATGACAG TATTAAAGG AGATAACTTA GAAATATTAA	720
AAACTATTGA ATCCTCAAGT ATTGATTTAA TCTATATGGA CCCTCCTTTC TTTACACAGA	780
AAACCCAAAA ATTATCTAAT AACAAAAATA TTATGTATTG ATTCGAAGAT ACGTGGAC	840
CGATTGAGGA TTACAAGAA TTTTGTCTG TAAGATTAGA AGAATGCAA AGAGTGCTAA	900
AAAATAGTGG CAGTATTTTC GTTCATGTG ATAAAAATGC AATCATCAT ATTAGATTAA	960
TTTTAGATAA TATCTTTGGA GTAGATATGT TTCAAGCGA AATTATATGG AACTATAAAC	1020
GGTGGCTAA TTCAAAAAAG GGATTATTGA ACAATCATCA AAACATTAC TTTTATTCAA	1080
AGTCAAAAGA TTTTAAATTT AATACAATTT TTACAGAGA TTCTTCTACT ACAAATATCG	1140
ACCAATATCT AGTGGAAAGA AACGAGATG GAACTCTTAA AACTATATAT AAGGTGATA	1200
ATAAATGTAA CTATATCTTA GCAAAAGAGA AAAATGGAGT TCCCTTTTCA GATTGTTGGA	1260

1257

ATATACCATT TCTTAATCCA AAAGCTAAAG AAAGAGTAGG TTATCCTACA CAAAAACCTA	1320
TTCTGTATT AGAACAAATT ATAAAGATTG CTAAGTATAA AATGATATA GTTTTAGACC	1380
CGTCTGTGG AAGTGAAGT ACTTTAGTAG CCTCCAAGAT TTTGAATAGA AATTATATGG	1440
GGATTGATT ATCTGAGGAA GCTATCAATA TAATCAGCA ACGTCTGAA AATGTTATAA	1500
AAACAAGTTC AATTTTATTG AATAAAGGAA TCGAAGCATA TAGAACCAAA ACTGAGGAAG	1560
AGGAAACAT TCTTAAATTA TTACAGGCAC AAATGTTCA AAGRAATAA GGAATTGATG	1620
GTTTTTTACC TAAACATTTT CAAAAAACC CGATACCTAT AAAAATTCAA AAAAATAATG	1680
AATGTCTGAA TGAGAGTATC TCTTTATTAC AGAATGCTAT AAATCCAAA AAACCTGATT	1740
TTGGAGTAGT TATAAAAACT CATTCG	1766

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CCGAAAAATCA AATTCAAACC ACGTCAACGT CGCCTTGCCG TACTCAAGTA CAGCCTCCGG	60
CTAGTTTCCT AGTTTGCTCT TTGATTTTCA TTGAGTATTA AACTAAATTA AATAATATTA	120
CGCGGAGAA TTTCTAATTC TTCCCTGGTC AAGCGACGCC ATTCCCTCTG TTCTAGGTTT	180
TCATCTAATA CTAAAGTTCC CATAGTCAAT CGTTGCAAGT CCACCACTTC CTTGCCACAG	240
TAGCCCAACA TAGCCTTGAT CTGATGAATC TTCCCTTCTG CAATGGTCAC ACGGATTTGG	300
CTTTGATTCT TTTCTGTATC TATGGATACA AGTCCAAGTA TAGCGGGTTG ACAGGTAAGG	360
TCTTTGAGAG GAATACCTC AGCAAAATGC TCCACATCTT CTGGGTTCAT GATTCCCTTG	420
ACTTGTGCCA GATAAGTCTT GTCCACATGA CGCTTGGGCG AAAGAAGAAC ATGAGCCAGC	480
TGACCATCAT TGGTCAAGAG CAAAAGACCA TGCGGTCTCA TATCCAAGCG TCTTACTGGG	540
AAAACCTCCT TACTCCGCGC CAAGTCATCC AACAGTCCA GAACGGTTCT GTGCTTGGGA	600
TCCTCAGTGG CTGAGATAAC TCCTTTGGGC TTGTTTCATCA TGATAGTAC AAACCTCTCA	660
TACTCCAACA CTGCCCCATC AAAGCGAATC TCATCTATTT TTTCATCAAT CTGCAATTTA	720
CGTGATTTTT CTTTTGACC ATTTACAG	748

(2) INFORMATION FOR SEQ ID NO: 237:

1258

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

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AAAAGATTAC ATTGCAACAA TTGAAATTA TCCAAAGGAA GGCATTACCT TCCGTGATAT      60
TAGTCCTTTG ATGGCTGATG GAAATGCTTA TAGCTACGCT GTTCGTGAAA TCGTTCAGTA      120
TGCTACTGAC AAGAAAGTCG ACATGATCGT GGGACCTGAA GCTCOTGGAT TTATCGTGGG      180
TTGTCCAGTT GCCTTTGAGT TGGGAATTGG TTTTGGCGCT GTTCGTAAAGC CAGGTAAATT      240
GCCACGCGAA GTTATTCTCG CTGACTATGA AAAAGAGTAC GGTGTGCGATA CCTTGACTAT      300
GCACGCGGAT GCCATTAGC CAGGTCRACG TGTTCTTATT GTAGATGACC TTITGGCGAC      360
AGGTGGAACT GTTAAGGCAA CTATCGAGAT GATTGAAAAA CTGTGTGGTG TTATGGCAGG      420
TTGTGCGCTT CTGTGTAAT TGGATGAATT GAACGGCGCT GAAAAAATGG GTGACTACGA      480
CTACAAAGTT CTATATGATTT ATTAATGAAA ACAGTCCCTA GGCGTGTTTT CTCTACACTA      540
GGATATAAAA ATAGACTATA ACTAGTTAGA GAAAACTAT AATTGAAAAA TATATCTTCT      600
TGCAGTATAA TAAAAGGACT AAGTGTTTGA GATTGTGCTT CAACATATG CAATTAITCC      660
TGAAGAGTAA CAGTTAGGAG AGGOTTATGC CGATTGGAAT TGATAAAAAA TTGCCAGCTG      720
TTGAGATTTT ACGGACAGAG AATATCTTTG TCATGATGTA TCACGCTGCT GCCCACCAG      780
ATATCCGTCG TTGGAAGATT TTAATTTTAA ATCTCATGCC ACAGAAAAATG GTACACAGAGA      840
CCCAGTTGTT GCGCCACTTG GCTAATACAC CCCTACAACG GGATATTGAT TTTCTCTATA      900
TGAGAGCCCA CCGTTCTAAA ACAACTCGTT CAGAGCACAT GGAGACCTTC TATAAAACTT      960
TTCTCTGAAGT CAAGGATGAG TATTTTGATG GGATGATCAT CACGGTGCTC CCAGTTGAGC      1020
ATTTACCATT TGAGGAAGTG GACTATTGGG AGGAATTTAG ACAGATGCTT GAGTGOTCTA      1080
AGACTCATGT CTATTCGACC CTTCATATCT GTTGGGGGGC TCAGGCTGGG CTTTATCTGC      1140
GCTATGTTGT AGAAAAATAC CAGATGGACA GTAACTATC AGGTATTTAT CCTCAGGACA      1200
CCCTAAAGAA GGGTCACCTT CTATTTAGAG GCTTTGATGA TAGCTATGTA TCCCTCATAT      1260
CACGGCACAC GGAGATTCTT AAGGAAGAGG TCTTAACAAA GACCAATCTC GAGATTTTAT      1320
CAGAAGGACC TCAGGTTGGG GTTTCTATTW TGGCCAGTCG TGATTTACGA GAAATTTATA      1380
GTTTGGGTCA TTTGGAATAT GACCGTGATA CTTTGCGAAA AGAGTATTTT CGAGATCGTG      1440
ATGCAGGTT

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1449

1259

(2) INFORMATION FOR SEQ ID NO: 238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 904 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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TACCCGCTTC TTCAAGAGT TGGAGCAGGG CTGTGTTGCG ATCTTTTGTC ATAGTCTCTC      60
CTTTTAACGG CGTTTCGAA GCACCTTATA GACAGCTAGT GCTAATGTAT AGTCTACCAT      120
ACTATGGATA ATTGTACCAA ATCCCACTAG TACAAATAGA ACATAAACA TATTTTCTAC      180
ATTGTTACCA GAAGTTGCGT AAAAAACGAC ACAGGCCAAT ACTTCAGCAA GGGCATGAAC      240
AACAGCCAAA ACAAAGTTGA AAATCCAGGA AGATTTGGT TTATCTAGGG TATCGGGGAA      300
TTTTTGTAGG TAAAGAGCTC CTAAAGCACC AAAAGATATA TGGGAAAAAG CCCGAAAAAC      360
GATAACCATG GGATAGCCAG CCATCAAAAA TCCAAAACTA GAGGCTAGGA TGACAAAAAC      420
TGCCATCAAG GCGCACAAGA ACATGGCTAT AAAAATAGCG ATGTGGCTCC CCAAAGTATA      480
GGAAGCAGGT GGAATGACAA TCTTGAAAGG CATAACAATT GGAATCAAAA TCGCAATAGC      540
CGTTAAAGG GCTGTCAATG TCATAAATTG TGTCTTTTTC CGTGATTCA CAAGAATCTC      600
CTTTTAACT GCATATACAC TAGTATGGTA CAATAAACA GACAATAAG CAAGAATTTA      660
CTTGGGTTTA TAGATCATTT TTTAGTTAAA AGTTATAGTA GATTGAACT AGAATAGTCC      720
ACCTCTACTT CTAACAATT GTTAGAATC GATTGGCTG TCCTGATCGA TTTGTCCGT      780
TCTTATTTTC TTTTACTATA GTAAAGATT CATTAAAAAG AAACGTGATA GAGCAAAATC      840
TCCACCTTCA GTTTGGAAA GCGGAGATTG TTTTATTATT TTTCCAGGGT TTGTAGTCGT      900
GGGA                                                                 904

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(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

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CACTCAACA TGACTTATAT CAAGACGGAT GGACTTCAAG ACGATGCCAA TCGCTTGAAT      60

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1260

CCTAACATTC AGTTTGGTGT TCGTGAATTT GCAATGGGAA CAATCTTGAA CGGGATGGCC	120
CTTCATGGTG GACTTGGTGT ATACGGTGGA ACTTTCTTCG TCTCTCTGA CTATGTGAAG	180
GCAGCTGTC GCTTGTGAGC CTTACAGGA CTTCTGTGA CTTATGTCTT TACCCATGAT	240
TCAATCCGAG TTGGGGAAGA TGGTCCGACT CATGAACCA TTGAGCATTT AGCAGGTCTT	300
CGTGTATGC CAAATCTAAA TGTTTTCCGT CCAGCAGATG CGGTGAAC CCAAGCAGCT	360
TGGTACCTTG CAGTGACAAG TGAGAAAACA CCAACTGCC TTGTCTTGAC ACGTCAAAAT	420
TTGACTGTG AAGATGGAAG AGACTTCGAC AAGGTGCTA AAGGTGCTTA TGTGTATAT	480
GAAATGCGAG CCGACTTTGA TACCATCTTG ATTGCGACAG GTTCAGAGGT TAATCTTGCT	540
GTCTCAGCTG CTAAGAATTT GGCTAGTCAA GGCGAAAAA TCGCGTACT CAGCATGCCA	600
TCTACAGATG TCTTTGATAA ACAAGATGCA GCTTACAAG AAGAATTTCT TCCAAATGCA	660
GTCCGCGTGC GTGTTGCGAT CGAAATGGGT GCAGTCAA ACTGGTACAA ATMTGTTGCT	720
CTCGATGGTG CCGTTCTAGG TATTGATACT TCGGAGCCTC TGCCCCAGCA CCAAAAGTAT	780
TGGCAGAATA TGGCTTTACT GTAGAAAATC TTGTAAAAGT TGTTCGAAC TTGAAATAAT	840
CTTAAATATC AGGGCGTAAG CTCTGTTTTT TCTTACCAGA AAAGTAAGGT ACAATCTGT	900
AAAAGTAGCT GAAATTTGAT ATAGTAGTCC TATGTAAAAG ACAAAG	960

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CGGGGCTCCc TAGTCTCTAG GGAGCTATTT TGTGTTTTC AAGAAGTTAT CTCTTGAT	50
TTTATATCTA ATGAAATCA AAGAGCAAGC TAGGAACCTA GCCGTAssTG CTCAAAACAC	120
TGTTTTGAGG TTGTAGATAA GACTGACAAA GTCAGGAACA CATATCTACG GCAAGGCGAC	180
GTTCAGCGCG TTTGAAGAGA TTTTCGAAGA GTATTAGTTG TGAATCTGGT GCAGTCGTCC	240
CAGATTATTC TTATTAGTAG GGTCTTGTTT TCTATATCCC CTCGTASTTA ACAAGACCTT	300
GAGCATTTTA GAAAGAGGAA TCTATGTCTA CGAAATATAT TTTGTAACT GGTGGTGTGG	360
TATCGTCCAT TGGGAAAGGG ATTGTGGCAG CGAGTCTAGS CCGTCTCTTG AAAAATCGTG	420
GTCTCAAAGT AACCATCTAA AAGTTTGACC CTATATCAA TATTGATCCG GGAACCATGA	480
GTCTCTACCA GCACGGGGAA GTTTTGTGA CAGATGACGG AGCTGAGACA GATTGGGACT	540

1261

TGGGTACTA	TGAACGTTT	ATCGATATCA	ATCTCAACAA	ATATTCCAAC	GTGACAACTG	600
GGAAAAATTA	CAOTGAAGTT	CTTCGTAAAG	AACGCCGTGG	AGAATACCTT	GGGCCAACTG	660
TTCAAGTCAT	TCCTCATATC	ACAGATGCTT	TGAAAGAAAA	AATCAAGCGT	GCCGCTCTAA	720
CGACCGACTC	TGATGTTCAT	ATCACAAGG	TTGGTGGAAC	ATAGGAGAT	ATCGAGTCCT	780
TGCCATTTCCT	AGAGGCTCTT	CGTCAGATGA	AGGCAGATGT	GGGTGCGGAT	AATGTCAATG	840
ATATCCATAC	AACCTTGCTT	CCTTACCTCA	AGGCTGCTGG	TGAAATGAAA	ACCAAACCAA	900
CCCAACACTC	TGTCAAAGAA	TTGCGTGGCT	TGGGAATCCA	ACCAATATG	TTGOTTATTTC	960
GTACAGAAGA	GCCAGCTGGT	CANGGAATTA	AAAATAAACT	GGCCAGTTC	TGTGATGTGG	1020
CACCAGAAGC	CGTTATCGAA	TGGTGGATG	TTGAACACCT	TTACCAAATT	CACTGAACCT	1080
TGCAGGCACA	AGGGATGGAC	CAAAATGTTT	GTGATCATTT	GAAATTAGAC	GCACCAGCAG	1140
CGGATATGAC	AGAATGGTCA	GCCATGGTGG	ACAAGGTCT	GAACCTCAAG	AAACANGTTA	1200
AGATTTCCTT	TGTTGGTAAG	TATGTGGAGT	TGCAAGATGC	CTATATCTCA	GTGGTCGAAG	1260
CCTTGAAACA	CTCTGGCTAT	GTCAATGATG	CAGAAATTA	AATCAATTGG	GTCAATGCCA	1320
ATGATGTGAC	AGCAGAGAA	GTAGCAGAAC	TCTTTGTCTGA	TGCGGACGGG	ATCATCGTAC	1380
CAGGTGGTTT	TGCTCAACGT	GGTACAGAAG	GGAAAAATCCA	AGCCATCCGC	TATGCGCGTG	1440
AAAATGATGT	TCCAATGTTG	GGAGTCTGCT	TGGGAATGCA	GTTGACATGT	ATCGAGTTTG	1500
CTCTGCACGT	TTTAGGTCTT	GAAAGTGCCA	ATTCTGCAGA	GCTTGACCA	GAAACAAAAT	1560
ACCTTATCAT	TGATATCATG	CGTGATCAGA	TTGATATTGA	GGATATGGGT	GGAAACCCTC	1620
GTTTGGGACT	TTATCCGCTC	AAGTTGAAAC	GTGGCTCTAA	GGCTGCTGCT	GCTTATCACA	1680
ATCAAGAAGT	GGTGCAACGC	CGTCACCGTC	ACCGTTATCA	GTTTAATAAT	GCGTTCCGTG	1740
AGCAGTTTGA	GGCAGCAGGT	TTTGTCTTTT	CAGGAGTTTC	TCCAGACAA	CGTTTGGTAG	1800
AAATCGTGG	AAATCCTGAA	AATAAAATCT	TTGTAGCTTG	TCAGTATCAC	CCTGAACGTG	1860
CAAGCGCTCC	AAACCGACCA	GAGAACTCT	CACTGCCTT	TGTTACTGCA	GCAGTTGAGA	1920
ACAGCAATTA	GCAAAATCAG	AACCTTTGAG	AAAAATCTCA	GAGTTTCTTT	GCATACGATG	1980
ATATTGCAGT	ATATCTGAGG	TAGGGGTCCCT	CTGTATGTAC	CTGCTACCGT	TGAAATCAAT	2040
AGCGACTCCC	TCTTGCCCTG	TGCTAGTGAA	TGATTTTATC	AGTATATTGA	AATGAAATAA	2100
AATTTGAACA	AATTAATTGG	GAAAGCCAAA	TCAATTTCTA	GCAAGTTT	AGGAACCTGGA	2160
TTGTATAGTG	AATGGAATA	AGATGTGAAC	ATCTCTATCA	GGAAAGTCAA	ATTAAATTTAT	2220
AGAAATATTT	TAGCAGTCAA	GATGTACTGT	TATAGATTCA	ATACATTATA	CTTTTTTAAT	2280

1262

TTAATCCACT ATAGTAAAT GAAATAATA CAGGACAAAT CGATCAGGAC AGTCAAAATCG	2340
ATTCTCAACA ATGTTTTPAGA AATAGAGGTG TACTATTCTA GTTTCATAT ACTATCCCA	2400
ATCATTCTA CCTCTCTCAA CTAGATGTAA CTTACAAAC CCCTGACCTC ATGAGCCACT	2460
TTCTTCCTCC TCATGAGGTC AGTTTACTT TCCTGCTGTC CAGTATCGTT TTCTCTGCT	2520
AGATTTCCTC AAAAGGGCAG ACTCCTCCCT TGGTGGTCA CACGATTTT TCATCTGAC	2580
TGTTCTTTAA TGCATCATTA ACGACGCTT TCTCTAGGT GGTTCATAAG GAACAGGAAG	2640
ATTCAGGTG ACTTTTCTAA TCCTAGAATA AAGTGTGAA AACAAATCG AATAAGCATA	2700
GAGACTAGAC AATTTCAGGA GCTGCTTGGC TCCTGTGCGA ACACATTTTC CCACCACGTG	2760
AAGA	2764

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCGTTTTTTT CATGTTTCTAG TACTACAACT TACGTTGTAG CGCCCTGCAC ATGCGTTCTG	60
CTTGTTTCTAG TTTCAAAGGT CTTTGTCACT TGCCTCTCTC AAGCGACAC TATATTAGTA	120
TATCACAACCT GCTTTGCTT GTCAACACTT TTTTGAAGAT TTTTAAGTTT TTTTAAACTT	180
TTTTTTCATCA AGTGGTCTG ACGCAACATA CCATAGTCCG TACGGGATTC GAACCCGTGT	240
TACCCGCGTG AAAAGGCGGT GTCTTAACCC CTTGACCAAC GGACCTGAGT TGTATTATTC	300
AACCTTACT ATATATACAGT CTTTTCAAAC TTTGTCACT ACTTTTTTAA ACTTTTTTTA	360
TTAATTTTAC AACAGCTTCA GTTCGAGCTG TATGTGGGAA CATATCGACC GACTGGATAT	420
AATGAAGATC ATAGACTTCT ACTAAGCGTA CCAATCACG AGCCAGGTC GAAACATTAC	480
AAGAAATATA AACCATTITT TCTGGTACAT AAGTAAGAAT AGTATCTAAT AACTATCAT	540
CCAGACCTGT ACGTGGTGG TCAACATCA AAGCTCTGC TCGTGGCTT TCCTGTGACC	600
AACGAGGAAT AATCTCTTCT GCGGTTCGAG CTTCTAATAG AGTATGTCA AATCCCATTC	660
TTTTAGCATT TGCTTGGCA CTTTCATAG CTTCTGGAAT AATATCCATA CCTCTGAGTG	720
TTTTTACTTT CTTTGCAGG GCAAAATCCAA TCGTTCCAA TCCACAATAA CGCTCAATCA	780
AATGGTCTTC TTTATCAACA TCCAGCGCTT TTAGTGCTTC GCTATAGAGG ACTTCTGTTT	840
GCTCAGGATT TAGTTGATA AAAGCTCGAG GGGATAGTA AAATTCATAA TTGAGTACAC	900

1263

CTTCTTGAAT	ACTCTCTGCG	CCCCAGATAA	TCTCTGTCCT	TTCAACCATAT	ATCTCACTGG	960
TTTTAGCTGT	ATTTGTATTA	ACAGCTACTG	TCACAACCTC	TGGGAAATCT	TTAAACCACT	1020
CTTTTACCAA	TTGAGTTAAA	TTAAGCTGCG	GGTTTGTAA	AAATAATAATC	TGAACCTGTC	1080
CGGCTTTTCT	CGCGCGTCGG	ACCATAATAG	TACCGACACC	TAGAACTTTT	CTCTCATCCG	1140
TGATTGGAAT	CTGGTGATAA	GTAAGTAATT	CTGCTAAGCG	ATTAGCAATC	ACTTGGGTTT	1200
CCTATCTTG	TACCAGGCG	TCTTTCAACT	CTACTAAATA	GTCAGAGTTT	TGTGCATATA	1260
AGCCCGCCTT	GACCTGATTT	TTAAATTTTC	GAGTCTGAAA	TTGTAACCTA	GCTCTGTAAT	1320
ATTTTGGTTC	CTGCATTCCA	ATAGTTGGAC	GAATTCATA	ATTTTCATAT	CCTGCAGGAG	1380
CAAAATTTTT	CAGCGCTTGA	TGAAGTAAGT	CCGCTTTGAA	CTCCAGCTGC	TTATCATAAT	1440
GCAGGTGCAT	GATTTGGCAG	CCTCGGCATT	CATTATAAAT	AGTACAAGAT	GGCACAATTC	1500
GAAATTTAGA	CTTCTTGTTG	ACCTTCAGTA	ATTTTGCTTC	AACAAAGTTG	CGTCTAATAG	1560
AAGTAATCTG	ACAATAGATA	TCTTCGCCCT	TGAGAGCTCC	TGCTACAAAG	ACTAATGTTT	1620
TTTGGTAAAA	GCCGATTCCC	TCACCGTTAA	TTCCCATGCG	CTTGATTTTT	AAATGGTATTT	1680
TT						1682

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TTAACTTTGG	TCAATCTTTT	AAAGTCATCC	TCTGTAAGCA	TGCTAACCA	TTGATGTTTC	60
CGTTTATGCG	TAAATCACC	AATTCGGACT	ACAGCTATAT	CTAAATCTTT	CCAACTATTT	120
TCTAAATTTT	CAAAATATCT	TGATTGCAAA	ATACCATCTG	CTAACAAATT	ATTTTCTTGC	180
ACAATCGTTG	CATTATAAAA	TGTACACTCT	CCATGAAATT	TTCTAGACAT	TTCTATAAATC	240
AGTGTATTCA	CATGGTATTT	AGCGTGATG	TGACTAGGAC	CACCTGCTAG	AGGATAGAAG	300
TGAACATTC	GGACATTTT	ACTGTGAATT	AAATCTACTA	AATTACTTAA	ACTTTTCCCC	360
CAAGAAAGC	CAATTTTCAT	ATTATCATCA	ATTAGATTCC	TAAGGACGCC	TGCTGCAACT	420
TGAGAAATTC	TTTCAGATAA	AAATGTTGGA	GTATCATCAA	ATTCATTTGG	AAATAATTTCT	480
AAACTTTTCA	AAGTATTTT	TTCTTTTACA	TAATTTTCCA	ACTTAAACAT	ATTGGTATCA	540

1264

AAATTCCTA TTTCAATTT AACAAATCCT ACATTCCTTG CTCTGTGTAA CATTCTACTA	600
ATAGAGGTTT TATAAATTC TAAATTTGCT GCTATTTGTG ACTGATTAA GTTTTCAATA	660
TAATACAGAT AAGCAATTT AGAAAGCAGT TTATTCCTAT CTGTATTAC ACACITAAAC	720
TCTTACGAAA CTACCTTAAC CATTATCCCA GCATTTTCTA ATGTAGCTAT ATTTTGTTTA	780
GAAAGTTTGT GGTCTGTAT TACTTCATAG ACTTGACTTA AAGCAAACT TCTTACTGTA	840
CCTCTTTTAT CAAATTTACT TGAGTCAGTT AGGACAATGA CTTTATCCGA CACTGCTGAA	900
ATATATTGAA CTACCTCACT GCGCATTAAA TCTTTTCCGG TAAAGCCCAT CTCTTTATCG	960
TAACCATCTG TCCCAACAAA AGCTTGACAC ACATGAAAG TCTGTATCAT TTCTTTTAA	1020
AAAGGTCCTA CAGTCACCTG TGAATCTTTC TGAAACTCAC CACCAGAAC AATAACACGA	1080
CATGAATCAT AAGCTCTCAC AAAATTTGCT ATAAAAACG AATTTGTATC AATCGTAACA	1140
TTTCTTTTTT GCTTGCATAT TTCTTCAGCA AGTAAGCAC AGGTGCATCC AGATTCCTATC	1200
ATTATTGTTT CATTATCTGA CACCAATTTT ACTGCTTCTT GAACAAATTT TCTCTTAGTT	1260
TCATAATTA TTAGCAAAAG TACATTTAAG TCATCTCCAC TATTTAATAC AGCATATCCA	1320
TGCTCTCTGT GTAATAAACC TTTTGACTCT AATTTATCTA AATCTTTTCT AATCGTTACT	1380
TTCTGATACAT TTAATTTTTC CGATTAATGA TTAACGTGTA TCTTTTCATA TCTGATACT	1440
AAATTAATTA TTTGTTCCAA TCTTTTCATT TTACACCTCC GTTTTATCTT ACCAAATATA	1500
AAAGCAAAAA ACAACAAAT AACCTTCTGT TCGTAATGT TTTTCTTTCG TTTTGTGTAT	1560
AGGATAGACT TATGAAGAGG AGGAATCTT ATGGAAATAT CTAAAGGAAT TATTTTAAAT	1620
ATTCAACACT TTTCAATTCA TGACGGTCCG GGTATTCGTA CAACGTGTTT TTTAAAGGA	1680
TGTCTCTGCG GCTGTCCATG GTGTTCTAAT CCTGAATCTC AAAGAAATGA ACCTGAAAAA	1740
ATGAAAGATG CTCAACGAGA GAAATTCACC TTAGTCGGTG AAGAAAAGAC TGTAGAAGAA	1800
ATTATTACAG AGGTATTAAA AGACAAAGAA TTTTACGAAG AATCCGGTG AGGTTTAACT	1860
TTATCAGGAG GTGAAATATT TGCTCAGTTT GAATTTGCTA AAGCATCTT AAAATCAGCT	1920
AAAGAACATC ACATACACAC TGCCATTGAA ACTACTGCCT TTGTTGATCA TGAATAAAT	1980
ATTGATTTAA TTCAATATGT GGATTTTATC TACACAGACC TAAACATTA TATTTCTATA	2040
AAACATAAAA AAGTGACTGG GGTTTTAAAT CAAATGATTA TTAATAACAT TCATATGCT	2100
TTTTACAAAA ATAAACTAT CGTTTAAAGA ATCCAGTTA TTCTTAATTT TAACATAGT	2160
TTAGAGGATG CAGAAAAATT CGTACTCTA TTTAACTCAT TAAATATCGA CCAAGTTCAA	2220
CTACTCCCTT TTCAATCAAT TGGTGAAAC AAATATCGTT TATTAATCG GAAATATGAA	2280
ATCATGGAA TCAACGCAT TCATCCGAA GATCTTATG ATTATCAAAA GGTATTTCTG	2340

1265

AACCAACATA TTAATTGTGA TTCTAGTTT ATTTCCTTGA AATGCTCTAG CTATTTGCAG 2400
 ATAACAAGCA TCTATAATAC ATACTTAAC TTTCAAAGG TTTAGCTAAA AAATTTTACG 2460
 CAAACCTTTT CTATTTTACC TTGCTCTAGA ATTTTAAAC TGCTATACTT ATCACAAAAA 2520
 AACG 2524

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

CGTGCTTGGG GGCTTCTGGT CAAAAGGAAA GTCAAGACAGG AAAGGGGATG AAAATTGTGA 60
 CCAGTTTTTA TCCTATCTAC GCTATGGTTA AGGAAGTATC TGCTGACTTG AATGATGTTT 120
 GGATGATCA GTCAAGTAGT GGTATTCACT CCTTTGAACC TTCCGGCAAT GATATCCAG 180
 CCATCTATGA TGCAGATGTC TTTGTTTACC ATTCTCATAC ACTCGAATCT TGGGCAGGAA 240
 GTCTGGATCC AAATCTAAAA AAATCCAAAG TGAAGTCTT AGAGGCTTCT GAGGGAATGA 300
 CCTTGGAAAC TGTCCTCGGA CTAGAGGATG TGAAGCAGG GGATGGAGTT GATGAAAAAA 360
 CGCTCTATGA CCTCACACA TGGCTAGATC CTGAAAAAGC TGGAGAAGAA GCCCAAATTA 420
 TCGCTGATAA ACTTTCAGAG GTGGATAGTG AGCATAAAGA GACTTATCAA AAAAATGCGC 480
 AAGCCTTTAT CAAAAAGCT CAGGAATTGA CTAGAAATTT CCAACCAAAA TTGAAAAAAG 540
 GCAGTCAGAA AACATTTGTA ACACAACATA CAGCCTTTTC TTATCTAGCG AAGAGATTG 600
 GGCTTAATCA ACTTGGTATT GCAGGTATCT CTCTGAACA AGAACCAAGT CCACGACAAC 660
 TAACAGAAAT TCAGGAATTT GTTAAGACCT ATAAGGTTAA AACGATTTTT ACAGAAAGTA 720
 ACGTTCTCTC AAAAGTAGCT GAAACTCTTG TCAATCAAC AGGTGGGTT CTTAAAACTC 780
 TGAATCCTTT AGAGTCAGAC CCACAAAAATG ACAAGACCTA TTTAGAAAAAT CTTGAAGAAA 840
 ATATGAGTAT TCTAGCAGAA GAATTAAGT GAGGAAGAA TGAATAATTA TAAAAAATAT 900
 CTAGCAGGTT CAGTGGCAGT CCTTGCCCTA AGTGTGTGTT CCTATGAGCT TGGACGTTAC 960
 CAAGCTGCTC AGGATAAGAA AGAGTCTAAT CGAATTGCTT ATATAGATGG TGATCAGGCT 1020
 GGTCAAAAGG CAGAAAACTT GACACCAGAT GAAGTCAGTA AGAGGGAGGG GATCAACGCC 1080
 GAACAAATTG TTATCAAGAT TACGGATCAA GGTATATGTA CCTCTCATGG AGACCAATTAT 1140

1266

CATTACTATA ATGGCAAGGT TCCTTATGAT GCCATCATCA GTGAAGAGCT CCTCATGAAA	1200
GATCCGAATT ATCAGTTGAA GGATTCAGAC ATTGTCAATG AAATCAAGGG TGGTTATGTC	1260
ATTAAAGGTAA ACGGTAATAA CTATGTTTAC CTTAAGGATG CAGCTCATGC GGATAATATT	1320
CGGACAAAAG AAGAGATTAA ACGTCAGAAG CAGGAACGCA GTCATAATCA TAACTCAAGA	1380
GCAGATAATG CTGTGCTGCT AGCCAGAGCC CAAGGACGTT ATACAAACGA TGAATGGTAT	1440
ATCTTCAATG CATCTGATAT CATTGAGGAC ACGGGTGATG CTTATATCGT TCCTCAAGGC	1500
GACCATTTACC ATTACATTCC TAAGAATGAG TTATCAGCTA GCGAGTTAGC TGCTGCAGAA	1560
GCCATTATGA ATGGGAAGCA GGGATCTCGT CCTTCTTCAA GTTCTAGTTA TAATGCAAAAT	1620
CCAGCTCAAC CAAGATTGTC AGAGAACCAC AATCTGACTG TCACTCCAAC TTATCATCAA	1680
AATCAAGGGG AAAACATTTC AAGCCTTTTA COTGAATTGT ATGCTAAACC CTTATCAGAA	1740
CGCCATGTGG AATCTGATGG CCTTATTTTC GACCCAGCGC AAATCAAGAG TCGAACCGCC	1800
AGAGGTGTAG CTGTCCCTCA TGGTAACCAT TACCATTCTA TCCTTATGA ACAAAATGCT	1860
GAATTGGAAA AAGCAATTGC TCGTATTATT CCCCTTCGTT ATCGTTCAA CCAATGGGTA	1920
CCAGATTCAA GACCAGAAGA ACCAAGTCCA CAACCGACTC CAGAACCTAG TCCAAGTCCG	1980
CAACCGAGCTC CAAGCAATCC AATTGATGAG AAATGGTCA AAGAAGCTGT TCGAAAAGTA	2040
GCGGATGGTT ATGTCTTTGA GGAGAATGGA GTTCTTCGTT ATATCCAGC CAAGGATCTT	2100
TCAGCAGAAA CAGCAGCAGG CATTGATAGC AAATGGGCA AGCAGGAAAG TTTATCTCAT	2160
AAGCTAGGAA CTAAGAAAAC TGACCTCCCA TCTAGTGATC GAGAATTTTA CAATAAGGCT	2220
TATGACTTAC TAGCAAGAAT TCACCAAGAT TTACTTGATA ATAAAGGTG ACAAGTTGAT	2280
TTTGAGGCTT TGGATAACCT GTTGAACGA CTCAAGGATG TCTCAAGTA TAAAGTCAAG	2340
TTAGTGAAG ATATTCTTG	2359

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1052 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TTCTTTCTGC TATAATCGTA TAAATACTT ACTTTAGGAG TTCTTATGAA AGTTGTTAAA	60
TTTGGAGGTA GTTCTCTTGC CTCTGCTAGT CAATTAGAAA AAGTTTIAAA CATGTCAAA	120
AGCGATTACG ACCGTCGTTT TGTAAGTCGT TCTGCGCTG GTAAACGCAA TCCTGAAGAT	180

1267

ACTAAGGTTA CGGATGCCCT GATTAAATAC TACCCGACT ATGTTGCGG TAACGATATT	240
AGCAAGAACC AAAGCTGGAT TATCGACCC TATGCTGCTA TGGTTAGTGA ATTGGGACTA	300
AAACCAGCTG TGCTAGAAA AATTCTTAAA AGCATTCAAC CCTTGGCCAC TCTTCTTATT	360
GAAGAAATG AATTCTCTA CGATACCTTC CTAGCAGCCG GTGAAAAATA CAATGCCAAA	420
TTGATTCTGT CCTACTTTAA CCAAAATGGT ATCGATGCAC GCTATATGCA CCTAGAGAA	480
GCTGGGATTG TGGTCACAAG TGAACCTGGT CACGCTCCCA TCATTCCATC AAGTTATGAC	540
AAGATTGAAG AATTGACAAA CACCAATGAA GTCCCTGTCA TTCTTGGTTT CTTTGGTGTG	600
ACTAAGGAAA ATCAAACTGT TACTTTCTCA CGTGGAGGTT CTGATATTAC AGGTTCTATC	660
ATTGCTGCTG GTGTCAAAGC TGACCTCTAT GAAAACCTTA CGGACGTTGA TGGTATCTTT	720
GCAGCCCAAC CTGGTATTAT CCACCAACCA CACTCGATTG CTGAGTTGAC CTACCGTGA	780
ATGCCCGAGT TGGCTATGC AGGCTTCTCA GTCCCTTCATG ACGAGGCTCT TCTTCTGTC	840
TACCGTGAAA AATTCTCTCT GGTATCAAG AATACCAACA ACCCTGACCA TCCAGGTACT	900
COTATCGTTC TAAACACAG TAATGATGAA TTTCCAGTTG TGGGAATTGC TGGTGACTCA	960
GGCTTTGTCA GCATTAAATC GTCGAAATAC CTCATGAACC GTGAGGTTGG APTTGGCCGC	1020
AAGGTTCTGC AAATCCTGGA AGAACTTAAC AT	1052

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 855 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

CCCTCGAAAA CTAAGCCGAT GAAGTCAGAA CACTTCAATC CTGTTCTGTA CTGGTGGGAA	60
AATCGTGAG AGATTCTGGA AGGTAAGTTC TACAAATCTA AATCATTAC ACCTAGTGAA	120
TTGGCTGAGT TGAATTATAA TTTAGACCAG TGTGACTTTC CAAAAGAGGA AGAGGAAATC	180
TTAAATCCCT TTGAGTTGAT TCAGAAATTAT CAAGCGGAAA GAGCAACTTT AAATCATAAG	240
ATTGATAATG TATTAGCTGA TATTTTGCAG TTGTTGGAGG ACAATAATG ACACCAGAAC	300
AACCTAAAGC AAGTATTCTC CAAAGAGGGA TGGAAAGGAA ATTAGTGCCG CAAAATCCCA	360
ATGACGAACC TGCAAGTGAA TTATTAAAGA GAATTAAGC TGAAGAAGA AAATCTATCA	420
GTGAAGGAAA AATCAAGCA GATAAAAAGG AAACCTGAGAT ATTTCTGGT GATGATGGGA	480

1268

AACATTATGG GAAGTTTGCT GATGGAAGCA CTCAGAAAT TGATGTTCTT TATGATATTC	540
CTGATACCTG GGAGTGGGTG AGGATAAAAT CAATTATTTG GAATTTTGGG CAAATATAGC	600
CAGAGAAATC CTTTAGGTAT ATAGATACGT CTAGTATTGA TAGAAAAAAG AACATAATCA	660
ACTACAAAA TCTACAATAT CTTTCACCTG AACAAAGGCC TTCCCGTGCT AGAAAAATTAG	720
TTTCGCAGAA TAGTGCTCTA TTTTCAACAG TTAGACCAATA TCTAAAAAAT ATTGCTGTAG	780
TTAGAGAACT TAAAGAGTAT TTGATAGCTA GTACAGCATT TAATGTTTTG GGATACTTTA	840
CTTAACGAAA CATAT	855

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 660 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TTTAGGAAGG CTATCCGTAA TTTTACAAG GATTAGATA TTACAGAGGA ACATTTAGAT	60
ATTATCAAAA GAGAGATGTT TGCGCAATTT TTCAGTAGCA TGAACCTCTT TGAATTTATT	120
GCAACGCAAT ATGATGCTTT TGAATATGGT GAGATAATTT TTGATTTGCC GAAATTTTAA	180
CAGGAATTA CTTTAGAGGA TGTCTTGAT GCTGGACATC ATTTAATAGA TGATGGTGAC	240
ATAGTTGATT TTACAATATT CCCATCCTAG TAACCTATTA TAATAGACAC TAGAAGAAG	300
GGATGACAAG TATGAGAAAA AAAACAATTG GAGAGGTTTT ACGATTAGCT AGAATCAATC	360
AGGGATTGAG TTTAGATGAA TTGCAGAAAA AGACAGAAAT CCAGTTAGAT ATGTTGGAAG	420
CAATGGAAGC AGACGATTTT GATCAACTTC CAAGTCCTTT TTACACGGCT TCTTCTTTGA	480
AAAAATATGC ATGGGCTGTT GAGTTAGATG ACCAAATTGT TTGGATGCT TATGATCTCG	540
GGAGTATGAT TACTTATGAG GAAGTAGATG TTGATGAAGA TGAGTTGACA GGTCGTAGA	600
GTTCAGTAA GAAAAAGAAG AAAAAAATAT CATTTTTACC TTTATTTTAT TTTATCTCG	660

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1805 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

CCGGTTGCAC AGGATCGTGC ATAGTCAACT CTCACAGTAT AGCATATCTC CTATTTTCCT	60
ACAGTAAATA ACACCTAAAA TGAAGCTTTT TCTTTTACTT TTTTCTGCCA AGAGGCAAAA	120
AGCATGCTGA GGTA AAAAAC GCTCATCATA ATAGGAACAC CAAGAATGGT CTTTTCATGA	180
TAGAAAATCG TCAAA TAGG TGA AAGACA ACGCCAAGGA CAAAC TACT AAGCAGGCTA	240
ACAAATATGA ATCTCTCACG CAAAAAGGA GTGTGCTTGG TCGGAAATA ATCTCCAAAA	300
GCCAGCATGG TCCGTTTGAT ATTCCCTGTC ATAAAAGCGT TATATAGGC AATACCCGAC	360
ACTTCTCCAA AAGCAGTTGT CACCAGTCCC ATACAGAAGG CCAAGGGCGG CACTAGATAG	420
ATATTATCCA CAGTTTGGCG CACAAAAGCA ATAAATGATTG ATAAGATTGC CAAGGGAATC	480
AAGGACAGAA TAGGTTTTTT CACAATCTC AATTTTTCCT TATAAATCGT TAATAAAAAG	540
ACTCCCATCA TAAACGCTAG CAAGGTGAGA ACCTTGTCCT TAACATCCGA AACATATATT	600
TTAAATTAATT CTACTGAAG AAGACAACA TTTCCAGTTT GTCCAGCTAC AAGGTAATTC	660
CCGCGAACAA TAAAAGTGTA AGCATCCACA TATCCAGCAC AAAACGTCAA AAAAAGTGCT	720
AACCTTTTAG ACTGACGTGA TATTTTTCCT ATAGGTAATA ACCTCATTTT ACCTCCCATT	780
GTATTTTCTC TTAGAAATAT TGTACCATTT TCTTTCTAAA AAATCGTAGG CTACCATTTA	840
GATTTTACTA TTAGCATAAA AATAATATA GACAACTATT TATCCAAAA TAGATAGATG	900
TAAATGTGTT GCAACAAAG CATACGAACC TTATAGTAAA TCATTTCCAT GAAACTAGAA	960
TAGAGCCCTC TTAGCAAAAA TCATTATTTT AATTTATTTT TAATCACTCC TTGACATANA	1020
TAACTCTCAC CAATAAAAA CTATGTCTTA AAAAAATGGT ATAATAAAT CAATACTTGG	1080
GCTTGATGGC TATGCTACTA ATAACAATTA GGAGAGAAAA TCAGGCACCT GTTAACAACA	1140
AGGATATACC CCTTGAGATG AAAGGAAGCT TAGAAATCTT ATGATGAACA TGCAAAACAT	1200
GATGCGCTCA GCACAAAAA TTCAAAAACA AATGGAACAA AGCCAAGCTG AACTTGCTGC	1260
TATGCAATTT GTTGGCAAT CTGCTCAAGA TCTTGTCCTA GCGACCTTAA CTGGCGATAA	1320
GAAAGTTGTC AGCATTGATT TCAATCCAGC TGTCTGTGAC CCAGAGGACC TTGAGACTCT	1380
TTCTGATATG ACOGTCAAG CCATCAACTC TGCTCTTGAA CAAATCGATG AAATACCAA	1440
GAAAAAATG GGTGCTTTCG CTGGGAATTT ACCTTTCTAA AACAAGGAG CTGAACAAT	1500
GCCTGTGAT AACAAGGCT AAGAAAGGTG CAAAAATGAC TCTATATAT TGTAGTGGG	1560
TAAATCCCT ATGGATATTA TGGAGCCTAT TTTTGTGTAG AAAAAAGTCC CATATGACCT	1620
ATAATGAAAA GCGACAAAA AACTCATTAG AAAGAATCAT ATGGAACAAT TACATTTTAT	1680
CACAAAATTA CTAGACATTA AAGACCTTAA TATCCAGATT TTAGACATCG TCAATTAAGGA	1740

1270

TACACACAAG GWAATCATOG CCAAACGGG CTATGAAGCT CCATCTPGTC CTGAGTGGG	1800
AAGTC	1805

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CTGCATCTAG TTGTTTCTC CCTACAGTTT TAGCTAGACA GATGGAGAT TATGATTAA	60
CGTCGCCGCG TTGGGGTTCG GATACAACCTA GTGAGCTTGA GAAAGAAAC TCCTCTGCTG	120
GAATTAATAA TANTGACAGC ACTGGTGGCG GTAAAAGGTT AAATACCTCT ATTCTAGCG	180
CCTATAGTGG CTCAGATATT ACCCGGTAT ATTCATTGGG GTCGGCTCT AGGATGTCA	240
TGTACTATAA TGGAGGTGGT GACAATTATA TTGGTTCTGG TACTAGATTA GCTATGGCGC	300
CACAATTTGG AAATCATGTA AGAATTCATA CTTCAGGTTT TTGGAATCCA GATTCTTATT	360
AACCTACTTG TCAGAGTAAG CCTAAAGAT GGTGATTGT GGGGTAGCA TGA AAAAAGA	420
ATGCTACACC CTATTTTAT TATAAGGAGG AGTAAGGATG GAATTTTCA TTGTAACTCT	480
TGTACGAGTC GTTCAATCAC CTCGATTITA TATGCTTTA TTTTGACCC TTCCTTGCA	540
GAGTTTAGGA AMTTCCCTTG CTTTCAATGG TATTTATAAA ATTGAAGGTT TATCGATTTT	600
TTTTGCCGCT TCTCTATTG GAGGATTTT ACCGATTAGC CTAGTAGCTG CACTTATCTG	660
TACACTGCCG TATTCTAGTC AGATAATAGA GGATGCTGAG AGTCATTTTC TAACAGACAA	720
ATTGTGTCGA ATTTCTAAAA AGAAGTATCT GGCTATTGTG GGTAGTACTG TAATTATTTC	780
TTCTTTTCTA GTCTTTTTC TCCCCTATT ATTATTATTA GGAATTAATC TTTTAGTGAC	840
TCCTTATCAG GAAATTTATA TTGGAGATTA TAGTGGTGCC TTAAAGAAT TATTTGATTC	900
CAATCAGTTT CTCTATAGTC TTGTAACGAC TCTCTGGTAT GGAGTTTGGG CGCCTGTGTT	960
CTCTATTTTT GGACTAGCTA GTGCTTTGCT AGTGAAGAAA AAAATAGGAG CTATTTTCAT	1020
CCGAGTGGCC TATATGATGG TTGTTGGTAT TTTTGGGCT ATTTTAGGGC TATCTTACTT	1080
AGAACTGTG ACAACGCTAG CTTTGGGATA TCAGAAAGAT ATCAGTCTTT CCTTAGTTAG	1140
TGCTCATCTT GCFTTTATTT TATTGTTAG TTGTTGGTGT GTTTATGTTA CATTTTTCTT	1200
ACATTACAGG GACTATGTAT AATGAACAA TTGTTCAAT TTTATAAAA AGATTTCTTA	1260
GCAGTATTGG TTTATTTAT ATTACTGCTA TCTGTGTTT TATCTAGTAC AGTATATTTA	1320

1271

TTGCGCLGTC GCCAATATTC AATCCATCCA AATGTATTAG AATGGATCTT AGTTTACTT	1380
CAAGATATGA CGACTGGAGT ATATTGCTTT CCGTTCACAT ATATATTGTT CTTTTTTTAT	1440
TTGATGAATA ACTATTTTAA TAGGTTGGAG TGTGCGATTG GTCTGAAATC AATTAAGCAC	1500
TTTACCAGTT TTAGTTTCAA ATTAGCAGCT CTTAGTACGG GGATTGCGAC GCGCACTTTA	1560
TTTTTATTGA TTTTCTTAAT TGCATTAGT AATGTTTTA GCTTCTCTTT GGAGATAAAG	1620
GAGGTTGATT TTTTAAGAGA ATTTTAIGGT ATAAGTATTG CAAACAATGC TAGTTTCTTT	1680
ACAGGATTTT TTTTCTCTTA TATAGCATAC TATTCTTTTT TATCCTTACT TACTATTAGC	1740
AGTTTTTCTT GTTTTAAAAA ATCAACATG AGCTTAGTAT TTCGTGTTAC TTTTTTAITT	1800
GTAGAACTCT TATTCTGGAT TTATCAAGTTG GACAATGGGA TAATTGGATT ATTGCCAATT	1860
TTTCAGTATA TGOTAAATTC CAATCGGTAT GCATTGATT ATTGGCTTAC ATTACTATCT	1920
ATCATAATTC CATTGACTGT ATTTTCTGTT CATGAJAAT GGAAGAGAGT GTAAAAAGTTG	1980
GAAATGGGAA AGTTAAGTAG TCACATGTGG AGGTTGAATC AGATAATCTA TACCAAGTAC	2040
TTTTGGGGTT ATGTTCTTTT TTGGATATTG ATTTGTTTAG GATTAATGGTA TTGTTTAGAA	2100
GGAAATGATA GACTTGTTAT AGAAATTTTA AAAGGCCCTA ATCTGAGTCA AAACTCTTTT	2160
TTAGTCTTAT CTATATGGTT GCTTCATTGG TTTATTATTC ATACATTTTT TCTAGCAGTT	2220
GTATATCGTA GAAGAGCATC CGATTTCITT ATGGAAGTGA TTCGATTTTC TTCTATTAAAG	2280
CTCTGGATTA GGTATCAGAT TTGGACCTGT TTCTTTATG GACTCATTTT AATCATGGTA	2340
AAAGTTCTAG TGATTCAATT TATGTTACAG TTACCAAACT GGGATATAAG AGTTTGTGTT	2400
ATAGTTGATT CTTTGAATGC TTGTGTGTTA GTCTTGTTTT GCTTTATGTT ATACGCACTA	2460
GGAGCGAATG TACAAATGAA CTTTGCTTGC GTTAGTTTCT TTTTACTCAT GATTGG	2516

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1364 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

CGGTGTTTT TTGTAAATTT TCTAGCACTT GTATGTTAAA ATAGATACAG GTGTTTCATTA	60
AACYAGACTA AAAACCTATT TAAGCAGGCA AAATGAAGAA ATACCAACAA TTATTTAAGC	120
AAATCCAGA AACCATTCAA AACGAGACTT ACGCTGTGG AGATTTCCTT CCTAGCGAGC	180

1272

ACGACCTTAT GGAGCAATAT CAAGTGAGTC GTGATACCGT CCGAAAGCC TGTCTCTCCT	240
CCAAGAGGAA GGATTGTATCA AAAAGATAAG AGGGCAAGGT TCTCAAGTCG TCAAAGAAGA	300
AACCGTCAAT TTCCCTGTAT CCAACCTAAC CAGCTACCAA GAAGTAGTTA AAGAAGTTGG	360
ACTGCGCTCT AAAACCAACG TGGTCAGTCT GGACAAGATT ATTATTGATA AAAAATCCTC	420
ACTGATAACC GGTTCOCAG AGTTTCGGAT GGTTTGGAG GTGTCCGCC AGCGTGTGGT	480
GGATGATCTG GTATCCGTC TGGATACGGA CTATCTGGAT ATGGAACTCA TCCCAATCT	540
CAGTCGCCAA ATTGCTGAGC AGTCTATCTA TTCTTATATA GAAAATGGCC TCAAAGTCT	600
TATTGATTAT GCTCAGAAG AAATCACCAT TGACCACTCA AGCGACGAG ACAAGATTCT	660
CATGGACATT GCGAAAGACC CTATGTCTGT TTCGATTAAA TCAAAAGTCT ATCTCCAAGA	720
CGGACGCCAA TTTCAGTTTA CCGAAAGTCG CCATAAGTTA GAGAAATTTA GATTGTAGA	780
TTTTGCAAAA CGCAAGAAAT AAAAGACTGA GACACCAGAT CTGAGCTTTT TTCGCTCTA	840
TAATATTGTT AGTGGTAAAC CCCCCTATGG ATATTATGGA GCCTATTTTG TGTAGAAAAA	900
AAGTCCATA TGACCTATAA TGAAAGCGA CAAAACAAT CATTAGAAAG ATTCAATATGG	960
AACAATTACA TTTTATCACA AAAGTCTCG ATATTAAAGA CCCAAACATC AAGATTCTAG	1020
ACATCATCAA TATGGATACC CACAAAGAAA TTATCGCTAA GCTGGATTAT GAGGCTCCAT	1080
CTTGCCCTGA TTGTGGAAGT CTAATGAAGA AATATGACTT TCAAAAACCG TCTAAGATCC	1140
CTTACCTCGA AACAACGTGT ATGCTTACTA GAATCTCTCT TAGAAAAGCT CGTTCAAGT	1200
GCTATCATTTG TTCTAAATG ATGGTGGCTG AAATTTCTAT CGTCAAGAG AAATCATCAA	1260
TTCTCTGTAT TATCAACCAA AAAATTGCGC AAAAGTTGAT TGAGAAAGTT TCTATGACCG	1320
AATATGCTCA TCAGCTGGCC ATTTCAACTT CAAGTGTAT TCGG	1364

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CCATGAAGAC CGCTTGAAT TCGAATGGCA CAACTTTTG TTGAATGGTC TATTCCTATT	60
GACATCGGF GGAGGAATTG GACAATCTCG TATGGCCATG TTCTACTCTC GCAAGAGACA	120
CATCGGAGAA GTGCAACAA GTGTTTGGCC TCAAGAAGTC CGCGATACTT ACGAAATAT	180
TTTTAGAGA ATCGAACCCG AAGGTTGGT TTTCTTCTC TTTTGTCTA TAATTTGTA	240

1273

TAATAAACAG TATGAAAATC GTATCAGGAA TCTATGGGGG ACCTCCCCTC AAGACACTAG	100
AAGGCAAGAC GACAAGACCT ACTTCGGATA AGGTTAGGGG AGCCATTTTT AACATGATTG	160
GTCCCTACTT TGAAGTGGGA CGAGTCTTGG ACCTTTATGC AGGTAGTGGT GGTTCATCTA	220
TCCAAGCAGT ATCCGCTGGC ATGTCACGTG CTGTTTGTGT GGAGCGAGAC CGTAAGCTCA	280
GACCATCGTG GCTGAAAATA TCCAGATGAC CAAGGAAGTT GGAAAATTTT AACTCCTCAA	340
GATGGATGCA GAAAGGGCAT TGGAAACAGT ATCTGGGGAA TTTCACCTCG TTTTCTTAGA	400
CCCTCCCTAT GCCAAGGAAC AAATCGTAGC AGATATTGAA AAAATGGCTG AGAGAGAGCT	460
TTTTTCTGAA GATGTTATGG TTGTGTGCGA GACGGATAAA GCCCTTGAC TCCAGAAGA	520
AATTGCCTGT CTGGGTATCT GGAAGGAAAA GATTATGGA ATTAGTAAGG TGACAGTCTA	580
TGTCAGATAA GATTGGCTTA TTCACAGGCT CATTGTATCC GATGACAAAT GGGCATCTGG	640
ATATCATGTA ACGGCGAGC AGACTTTTGG ATAAGCTTTA TGTGGGTATT TTTTAAATC	700
CCCACAAACA AGGATTCTTC CCTCTTGAAA ATCGTAAACG GGGGTAGAA AAGGCTGTGA	760
AACATTGGGG AAATGTTAAA GTCTGTCTCT CTCATGATAA ATTGTGGTGC GATGTCGCAA	820
AAAGACTGGG GGCTACTTGC CTAGTGGCAG GTTTGAGAAA TGCCTCGCAT TTGCAATATG	880
AAGCCAGTTT TGATTACTAC AATCATCAGC TGCTTTCTGA TATAGAGACT ATTTATTTAC	940
ATAGTCGACC TGAACATCTC TATATCAGTT CATCAGGCGT TAGAGAGCTT TTGAAGTTTG	1000
GTCCAGATAT TGCTGTCTAT GTTCCCG	1060

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3652 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

CCGGTCAAGT TAAAAAGGCT ATTTCTTCCC ATTTTATTTA TTTTTTAGGA GTGGTAACGT	60
ATCAAAATAG CCCAAGGCTT CTCACCCGTG TGAGTTTGAA TAATGGAACC GCTTCCAAA	120
ACAGAAATG GCTTTTCAAC ATAAGCTTGT AAGCTTCTT TCATCTCTT TGCCCAATCA	180
TCATACCAAG AATATGAAT TCCAATCTCT GCTACAGCAC GTTCAGAAAG CGATGTTATC	240
AATCATCTA ACCATTTTTT AAATGTTTTA GTTCCACGAC CTTTAACCAT TGGCTGCAAT	300
TCATGGCTT TCAATTGCA TACAGCAGG ATATTGAGAA GAGAGCTCAA CAAGCCAGTT	360

1274	
ACACGGCTAA TFCGTCCACC TTTCACAAGA TTTTCCAAGG TTGAAACACC AATATAAAGC	420
TCNGTATGCT TTTTAACCTC TCTACATGA GATAAAATGG CCTCCATATC TTTACCTTCT	480
TGAGCTAACT TCGCAGCCTC AACCACTGG AATTTCAGGG CTTGTCTAGT GAAGGAACTA	540
TCAACCAACG TCACATCTGC AGTAGATAGG CTAGCACCTT GGCCTGCTGC TTCTACCGTA	600
CCCGAAGAGC CATTGAGCAT ATGAATAGCA AGAATCTGGC CACCATCTTT GCATAGGTCT	660
TCAAAAATCT CAGCAAGAC ACCTACAGGT GGCTGACTTG TTTTCGGAAG ATTCTTACTT	720
TCCTGATCACT ACTGAAGAAA TTTACCTTCT TCTTTCAANT CCGCATCAGA ATAAACAACA	780
TTATCAATCA TTACAGATAA TGGAACAATT GTAATATCTA ATTCGCTTAC TAGTTCAAGT	840
TCAATAGTAA CAGATGAATC GGTACAAATC TAAATTTTIG TCATAGTATC AATCTTTCTA	900
TTTTAGGATT CAGATTGGTT TCCTTACTTC TAATATATATC AAAAAAAGA TTAATAATCC	960
TAATGGAGTC AATCAAAATT TCCGTAAANT TTGATATATAT CAACCTATAA GAAAGAGGT	1020
GTCTCATGAT TAAAAAATTT TACCCCATTT TPACCAATTT ACTAGGTGCT GCTATTTATG	1080
CTTTTGGACT GACTTATTTT GTAGTTCCCTC ATCATCTCTT TGAAGGAGGG GCGACAGGCA	1140
TTACCTCTAT CACCTTTTAT CTTTTTAAAA TCCTGTGTTTC CTTGATGAAC CTGCTGATTA	1200
ATATTCCCTC TTTTATCTTA GCTTGAAGA TTTTGGAGGC CAAATCCCTC TATTTCTAGTT	1260
TACTAGGAAC CTTAGCTTTG TCCGGCTGGT TAGCTTTTTT TGAGCATATP CCCCCTTCTA	1320
TTGATCTTCA AGGTGATTTA CTAATCACAG CCTTATAGC GGGAAATCTTA TTGGAAATG	1380
GCCTTGGAA TATTTTAAAT GCTGGAGGTA CAATGGCGG AACTGATATP CTAGCTGCTA	1440
TTCTCAACAA ATACACTCAT ATATCCATAG GAAAACTGCT CTTTATCTTA GATTTTTGTA	1500
TTCTCATGTT GATTTCTCTA ATCTTCAAGG ATTTGAGATT GOTTTCCTAC ACGCTTTTGT	1560
TTGATTTTAT TGTTTCTGTT GTTATTTGATT TGATTGGTGA AGGAGGATAT GCCGCAAG	1620
GCTTTATGAT TATCAAAAA CTTCTTGACC AACTTGTAA GCGGATTAAT GATGACCTCG	1680
GAAGAGGTGT TACTTTTATT TCTGGTCAAG GCTACTATAG TAAAGAAAAA TTGAAAAATCA	1740
TCTACTGTAT TGTGGAAGA AATGAAATTT TGAAAACGAA GGAATGATT CATCGAATCG	1800
ATCCTCAAGC CTTTATTAAT ATTACAGAAG CCACTGAAAT CCTAGGAGAA GGCCTCACCT	1860
TTGAAAAAGA ATAAAAAGAG GTAATGTGCT GACCTCAAAA GTTAGACTAA ATCATCTATC	1920
TTTTGGGTTA CAGACAACCT CTTTTTATTT TTAATTTACTC AAGCTCTTAA GACCAATCC	1980
GAGTTACTTC TTTCATCAGCC TTTAACTGAT CCACTAATG GTCAACTGAG TCAAAATTTGG	2040
TCATATCTCG AATGCGATCA AGCCAAATAA CCAATGACGT TTCCCATATA ATATCTTGAT	2100
TAAAAATCAA AATATTGACT TCAAAACGTG CTCTCTCTCC ATCAAAGTCA ACATTTTTC	2160

1275

CGACACTAGC CATAGCAGCA TACTTCTGTC TTGGAATCTC AACATCAACA ACATAAACGC	2220
CATCTGCTGG CATATAAGTA CGGTCTAAAA GCACATAAAT CGCTGTCGGA TAACCAATTG	2280
TAGCACCAGC AGCATTACCA TGAACCAACA TACCTCTTGA TGGGAAGCGT GCCCCCAAAA	2340
GTTTTCCTGC TTCTTTUACA TTTCATCTA AAATAGCTTG ACGGATACGA GTTGAACFAA	2400
TCTTTCCTTT CTCATCTTCT ACAGGTGGAA CAATGATAAC TTCTCCATCA AAGTAATTCT	2460
TTAAATCTTC TGCTGTTTIT TTGTCAGAAC CAAATGTATA ATCAAAACCT GCAACAATAA	2520
TTTGGGCATT CATAGCCTTG ATATAAGTTG CAAGAATTC TTGTGCAGTG AGACTAGCGA	2580
ATTGACTACT AAAATCAAGG AGATATAAAT CTCTACACC TTCGCGCTTT AATTTCTTTT	2640
CACGTTTCAGC AGGGTTCAAA ATATGCAGAA ACAAACTGG ATGATAAGGC TCTAAAGCGA	2700
TCTTTGAGAG TTCATTAAAG GTCATAACGA CGATAGGCAJ CAAATCCTTT CTCGCAGCCT	2760
TGTTGGCAAC ACGAAATAAT TCTTGATGCC CCTTAGTAT GCCATCAAAA TAGCCGAGAA	2820
CAACGACTGA ATCAGATGGT GTGCCAATAT CTTTGTGGTT TTTTATAGGA ATAGTAATAA	2880
TCATAAAATA ATTATATCAT AGCGATAGCT ATTTCTGGAA CAGAAAAATCT GAAATGTTGT	2940
TTTTTTCACA TGAAGTGTAAC CTGTTTTCAA AAAGCACTTT ATTCTATCGT TGCTTAACTA	3000
TGAACTTTGC AATATCTTTC TCAAAAACCT GTAGGACATC TTCAAAATTT TGCAAGGAGT	3060
GATTAGACTT GTTCGGTAAC CATAAAGTGT CATACTATGC TTATGTATGA AAAAGCAATG	3120
CAACTAATCT CTGAGAACTT TAAATTTACTA ATTGGTGCCG AAAAGGTAGA ATTTAGAAATC	3180
GAGGTACACC TATGGCTGTA AAATTTACAA AATGAGACAA CTGCGGCAAG ATGTTTGAAG	3240
AATTTCTTAA ACTCCCTGAT TTGAAGCAAG TCACCTTCCC TAATGACAAA GAAAAAAGCC	3300
AAAACAGCAA AGAAAACTA GATGACTGCT TTCCAACAAC TCCCATCTAG TGTGCTTCAG	3360
ACTGGGCTAT TTTTCTCTCC ATCTGTTAGC TTGGATTCTC AGACCGTTTC AGCTAAAGAA	3420
TATCTTTTCC CTTATCAGAA GGAACGGCTC AAGCCATTCA GACAAAGTGA GGCACGACAA	3480
GCCATATTTT GAAACCAGAT AGCAGTCTTT ATAGTCAATT GAAATAAAAT CTGAAGAAAT	3540
CGAGTAGGAA ACTCATATCA ATGTTTAAACA GTGTCTTAAT CCAGATTCAT ACTCAATGAW	3600
AATTAAAGTG CAAACTAGGA AGTTAGCCGC AGGTATACAT TTGGGTACGG CA	3652

(2) INFORMATION FOR SEQ ID NO: 252:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 743 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

1276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GTACCGTGTG GCCAAGTAC AGCAAGGTTG GCTTTTGAC AAACAATACC AATCTTGGTT	60
TTACATCAAA GAAATGGAA ACTATGCTGA TAAAGAATCG ATTTTCGAGA ATGGTCACTA	120
TTATTATCTA AATTCGGTG GCTACATGGC AGCCAATGAA TGGATTTCGG ATAAGGAATC	180
TTGGTTTAT CTCAAATTG ATGGGAAAT GGCTGAAAAA GAATGGGTCT ACGATTCTCA	240
TATCAAGCT TGGTACTACT TCAATCCGG TGGTTACATG ACAGCCAATG AATGGATTTC	300
GGATAAGGAA TCTTGGTTTT ATCTCAAACT TGATGGGAAA ATAGCTGAAA AAGAATGGGT	360
CTACGATTCT CATAGTCAAG CTTCGTTACTA CTTCAAATCC GGTGGTTACA TGACAGCCAA	420
TGAATGGATT TGGGATAAGG AATCTTGGTT TTACTCAAA TCTGATGGGA AAATAGCTGA	480
AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC TACTTCAAA CTGGTGGCTA	540
CATGGCGAAA AATGAGACAG TAGATGGTTA TCAGCTTGGG AGCGATGGTA AATGGCTTGG	600
AGGAAAAACT ACAATGAAA ATGCTGCTTA CTATCAAGTA GTGCCGTGTTA CAGCCAATGT	660
TTATGATTCA GATGGTGAAG AGCTTTCCTA TATATCGCAA AGTAGTGTCG TATGGCTAGA	720
TAAGGATAGA AAAAGTGATG ACA	743

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TTTGTGGTTGA TGATACGAGG GATTGGTGA TTCTCTTGA CGATAGAAGT TTCAGCGACC	60
ATCATTTTTC AACAGTGATA GCACTTGAAT CGACGCTTTC TAAGGAAGAT TCTAGTAGGC	120
ATACCAGTCG TTTCAGATA AGGAATTTTA GRAGGTTTTT GAAAGTCATA TTTCCTCAAT	180
TGGTTTCCGC ACTCAGGGCA AGATGGGGCG TCGTAATCCA GTTTGGCGAT GATTTCCTTG	240
TGTGTATCCT TATTGATGAT GTCTAAATC TGGATATTAG GGTCTTAAAT GTCTAGTAAT	300
TTTGATATAA AATGTAATTC TTCCATATGA TTCTTCTAA TGAGTTGTTT TGTGCGTTTT	360
CATTATAGGT CATATGGGAC TTTTTTCTA CAATAAATA GGCTCCATAA TATCTATAGT	420
GGATTTACCC ACTACAAATA TTATAGAACC GAAATAATT T AATTAGAGAG CCAACTTTCT	480
AATATAGTAA TCGCGTCATA ACAAGGTATC TATCATTCAT GGAGTTCCTC CTGTATATCTA	540

1277

TTAGTAAAGT AAAACFATTT GAGGATATTT TAATGCCACA ACCTATTTGTT CCTGTAGAGA	600
TTCCACAATC TCGTCGTTTT GATTCCTAAAA AGAGAAATGA TATTCCTGCTT AAAATTCGTA	660
TTGGCAAGCT TGAAGTAACT TTTTTCATAT CTCTCAATCT CGAAATGGTA GAACAGCTTT	720
TGGATAAAGT GTTGTCTAT GACAATTCAT CTATCTAGCC TAGGGCAGGT CTATCTCGTA	780
TGTGGGAAAA CGGATATGAG GCAAGGCAAT GATTCATTGG CTATCTGCTT TAAACCCAC	840
TTTGAATTAG ATCCTTTCTC CGGTCAAGTT TTCTCTTTT GTGGTGGACG TAAAGCCCG	900
TTTAAAGCCC TTTACTGGGA TGGTCAAGGA TTTTGGCTAC TATATAAACG CTTTGAGAAC	960
GGAAACTGA CTTGGCCAG TACAGAAAAG GATGTCAAAG CTCTCACACC TGAACAAGTA	1020
GATGGCTTA TGAAGGGCTT TTCTATCACT CCAAAAATGA ATTTATCAGA AAGTCGTGAT	1080
TTCTATTGAA ATGAGGACTT TCTTTTGTAG TATAATAAAG TTAGGAATA AGGAGAGAA	1140
GCCCATGGAA GAAGATTGAA AATCATTCAA CAACAGAGTG CTACAAATGA TAGTCTCACC	1200
AATGAACCTG CCGTCTTCG TGAACAAGTG GCTTATCTAA CGCAAAAGCT CTATGGAAAA	1260
TCCTCTGAGA AAAGTGTTG CCCATCTGGA CAATCACTC TTTTGAAGA GGAACAAAAAT	1320
ATGGAAGAG ACTCTGACTT ACCCAGTTGA AAGAGAAGAA ATCCACTATA AAGCTAAGAA	1380
AGCTAAAGGG AAACGTCAAG CTCTCTCTGC CCAATTTGAT TCAGAAGAAG TTCATCATCA	1440
AGTAGAAGAG AGCATTTGCC CTGATTGTCA GGGAGATCTA AAAGAGATPG GAGCAACCT	1500
TCAAGACAA GAATTAGTCT TTATTCCTGC GCAATTAATA CGAATAGATC ATATCCAACA	1560
CGCTTATAAG TGCCAAGCAT GCAGTGATAA AAATCCGAGT GATAAAAATCG TGAAAGCTCC	1620
TATTCCTAAA GCGCCCTTTGG CGCATAGCCT TGGCTCAGCT TCTATTATCG CTCACACCAT	1680
CCATCAGAAG TTTAATCTGA AGGTACCCAA TTATCGCCAA GAAGAAGATT GGGCTAAGAT	1740
GGGTTTACCA ATCACACGTA AGGAAATTC TAATGGCAT ATCAAGGCGA GTCAATACTA	1800
TTTGGAGCCC CTTTATAATC TTTTACGAGA AAAGTTGTTA GAACAAGCTC TTCCTCATGC	1860
GGATGAACCC TCTTATCGGG TTCTAGAGAG TGATAGTCAG TTGCGCTTACT ATTGACTTTT	1920
TTTGTCTGGG AAAGCTGAGA ATCAAGCAAT CACGCTGTAC CACCATGATC AGCGTCGGAG	1980
TGGTTTAGTA GTACAAGAAT TCCTAGGAGA TTATCTGGC TATGTTTCAAT GTGACATGTT	2040
GCGGAGTAA CTTAGGACTT TAGTCTCTTA GTTCTGCTTA TCGGATAGCA GTCCAAGGTT	2100
TAGGATTAAG GCGACGCTAA CTTTGTGATA CTGCGAACAG CTAGAAGCTT ATCCTCAACT	2160
GGAGAAGCT GCATCTGTTG GATGTTGGGC GCATGTGAGA AGGAAGTTTT TTGAAGTGCC	2220
CCCCAAGCAA GCAGATAAAT CATCTTAGG AGCTAAAGTT TTAGCTTATT GTGATCAGTT	2280

1278

ATTTTCCTTG GAAAGAGACT GGGAGGCTTT GCCAGCTGAT GAACGACTAC AGAAACGTCA	2340
AGAAATCTTC CAGCCCCATA TGGAGAGCTT CTTTGCCTTG TCCCGCCGTC AGTCAGTTT	2400
AGCAGGTTCA AAATAGGAA GGGCAATTGA ATACAGCCTC AAGTATGAAG AAACCTTTAA	2460
GACTATTTTG AAGACGGAC ATCTGGTCTT TTCCAATTAAT CTAGCTGAAC GCGCAATTAA	2520
ATCATTTGGT ATGGGACGGA GTAAAGAAGT CCAGTGGACT CTTTTCAGCT GAGCTCAGTT	2580
TAAAAAGCG AGGGTGCTTA TTTTCTCAA GTTTTGAAG AGCTAAAGCA AGAGCTATTG	2640
TTATGAGCTT GTTGGAAACA GCTAAACGTC ATCAATTATA GTGCTTTGAA TCTATAACAG	2700
TACGCATCGA CTGCTAAAC ATTTCTATA ATCAATTTC TTTTCTTAAT CGATTTGTTT	2760
ATATCTTATT TCAATCCATT ATAAATAGCG AGAAATATCT ATCTATCTT CTAGAAATGC	2820
TTCCAAACGA GGAACCTCTC GTAAACAAAG AGGTTTGAAG GGCCTATTTA CCGTGGACTA	2880
AAGTTTACA AGAAAGTGC AAATAAGAAA TCTCCAGATT AGGAACATC CGTGAGTTCT	2940
CTAGTCTGGA GATTTTTCAT TAGACTTCGT TATTTGGACG TTACAATTAA TTATATGAAA	3000
ATCCCATATT ATTCTCAAT TCTATATTTT ACCTTTCTAA ATGTATAGAT TAACATCTTA	3060
ATTATAGCAT ATACGCGAA TTCTTTTCAA TCGTATGATT TACTGCATTA AATTAAAGTAA	3120
AAAAATTAAG GCAGTCCGAA GACTGCCGAT ATTTATCTCT CATCTCTTTA ATTTAGGTAA	3180
GTAAATTAAT AATTTCCCTA AAGATATGGA AATTATTAAAT ACTATAAATA CATATTATTA	3240
AGTTTATAAA TACTGTAAAA ATCCTGAAGT TAAATTTCTA ATAAATATCA ATATGTGTTA	3300
GTATCTTTTA AATTTTTAGA CAATTTACTA GTTCTATAGA CATGTTTAA AGACTCTATT	3360
TTACAATTCA AAAATTTTAT CTGCCACTTC ATTTAAAAAT TCTATATCAT GGGAAACAA	3420
AAAAATTAAT TTATCCATGG TTTTATACTT ATTAATCAGT TCAGATATTT TTATCATATT	3480
GGAATAATCC ATACCACCTG AAGTTTCTG TAAAAAGACA AATGGAGAAT TCTTGACAT	3540
AACAGATGCT ATTGCAAGCC TTTGCTTTTG CCTTCTGAT AAATCATCG GATGCCTTTC	3600
AATTAATTCG TCCAGGCATA AATCTTTTAA CCCAAATCAT TCATACCTCT CTCACATAGA	3660
TGTAACCTAC AAAACCCCTG ACCTCATGAG CCACTTCTTT CCTCTCATG AGGTCAGTTT	3720
TACTTTCTGC TGTTCAGTA TCGTTTTTCC TCGTAGATT TCCTCAAAAG GGCAGACTCC	3780
TCCTTTGGTT CGTCACACGA TTTTTCATC TCGACTGTTC TTAAATGCAT CATTAAACG	3840
GCTTTCTTC TAGGTGTTT ATAAGGAACA GGAAGATTCA GGTTCAGTTT TCTAATCTTA	3900
GAAATAAGTG CTGAAACAA TTCCGAATAG GCATAGAGAC TAGACAATTT GAGGAGCTGC	3960
TTGGTCTCTG TTCGAACACA TTTTCCACC ACGTGAAGAA AAAGATGGCG	4010

(2) INFORMATION FOR SEQ ID NO: 254:

1279

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

ATGCATCCGT TTGCAAGCC TAAATTGTAA TTTTTTCGA TTAAAAACAG AAAAAACCAG	60
GAAAAATGACA TAAAAATATC ATTCTTAGGC CTATTTATGC TATTTCTCTC TGAAAAATAT	120
GAGTATTCAG TCGGTCAAAAT GAAGCTGAAC GAACTCATTT TCCTCGCCT AATTCATGA	180
TTCGATGACA TTGTGGGCT ACATAAGCAT CGTGGGTCAC GATAATGACT GTTTTCCCTT	240
CTCGATTTCAT CTCTAAGAGA AACTTCAAGA CCAAACTCTCT ATTTTCAGGA TCCAGAGAAC	300
CTGTGGTTTC ATCGGCTAAA ATCAGCTGGC TGGGTTTTAA GATGCTCTA GCAACTGCAA	360
TTCTGTGTTG TTCGCCCCCA GACAACTCGG AGACCCCTTG ATGCAAAGTA GCTGATAAAG	420
CTACTCTCTC TAAAACTCTCT TCCACCTTTT TGAGCTTGTC TTCTTAGGC AATTTACAT	480
ATTTTCAGGC CACATGAGAT TGTACTCGAC CGTTTCATCA TCAATCAGGG CAAAAATTG	540
AAACAGATAA GAGATATGTT CACGGATTAT TGGTTGCGAC TTAGCAGAAAT TAACCGCTAG	600
ATTTGTCTGA CCAAAAACTCT CATACCGTCC GCTATAATCA CCATCTATCA AACCCAATAA	660
ATTTAAACAG GTCGACTTCC CACTACCACT CTTACCAACA ATAGCTACCA AATCCCCCTG	720
ATCAATCCTG AGAGATAAGT TATCCAAAAAT CACTTTTCCC CCAATGCTTT TGATAATATT	780
TTTCAACTCA ATCATAAAGAT GCCCCCTTTC AATAACTCTA CTAGACTTCT TTCTTCCATC	840
CTAGAAGCTA AGCCTAGCAC AAATAGTATA TCCAGACATG TAAAACTGC AAACAGTAGA	900
AGTGTAAAGA ACGCATGGGC AAAGAAAATC AAGACTAGAA GAGGGAAACT ATAGCCCAGC	960
AAGAGCAGAA CGAGGAGAGG ACGGTAGCGA TCGACCAATT TCCACCCCAT AAATCTCTTG	1020
GTAATGATAT CCCTCGCTT CAATAAGAAA GTTGTACTA GTAAGAAGTA GGAATCATC	1080
ATGCTAAGGA GACCAACAA AGCAAGAGT AGGTTAAAT TCCGAACAGC ATCTCGATAA	1140
GAATCCACTT TCTCTTGTTG AATGGCTTGA ATAGATGAAA ATTTTAAATA ATTTCCATCT	1200
GACAATTTCT CAACTAATC TGTAATCTCT TTTTATGTT GAACCGTATT TTCAATTTTA	1260
ATCGATTAT TTAAGCCAGT TGGTGACAGG GAGGCTTTCT CATCCACAT CATATCAGAA	1320
TCATTGACCA AGCTAATAAT TGGATTGGAG AGATTTTCTT TTCGCTTATC ACTATATGGG	1380
AAAAATGACC AATCTCTTTC ATAATAGGCA ATCTCGACAT CCATCTCTCT TATCGTTCTG	1440

1280

TTTGTGCTGCT CTTCATACIT CATCGAATGA AAGGCAATTA ACTTCCCCAA GAGCTGATTT	1500
TTATCTTCTT CACCTTTTGT ACTTGTGTGG ATCAAAATTA CTTTTAAAT ACCGGTATTT	1560
GGTAGCTTGA ATCCCTTGCT CTTTAGAAAA TTGGGATTGG CATGATAAAC ATCCACCGTA	1620
TCTGTAACT GATATTGCTG AATCTGTCTT GATTGGACAA AATTTTTTAC AGGAAGACTG	1680
CTACTCTGCA CATAGCCGCG CTGGGTTTTT TGTACCAAAAT CCGTATAAAA TCGATAGAAA	1740
TAATCTGTAG ATTTCCCTGA CCTGTGTAGC TCTCTTGCC ACAGATTATC ATTGAGTTTG	1800
AAGGTTTCTA AGGTCAGGTA ATTACCTTGA CTTACCCACT GTTGCTGATA AGCAAGTTCT	1860
TTGTTTTCTT GTTCTAACT TCTGCCACC CCAATCAGTA AGGCCGTCAG TAAATAGTT	1920
GTCCCTATTT TCATCACATA ATTGAAGATA AGACCAAAAT TGAAAGATGA AAAACCTTTC	1980
AGCAGAGAGC TGATTGTCTAT TTTTGGATT AAGAGTTAAG TCAACCAACT GATAAAGAGA	2040
TAAAGCTGCA ACAGCAAAAA ATGAGACAAC CACAGCATAG GAAACAAATC TTTTGGCTTA	2100
TAATCAAGCA AGAAAAACAC GCTTAGATTG ATCAACAGAG CCCCACCTAG GAGGAGGTAA	2160
AGGTTGCCTT TTACAACATC AGCTAAACCA GCCCTATCTT GAAACCAAG TAATTTTTGT	2220
ACCCCAACTC TTTTCATCTC CATCATGGT TGATACACTG TCACCTAACAC AAGAAGCAAA	2280
ATAGCCAAGA CAAAAACAAT GGCAGATAAA AGCAAACTCT GATTATGAC TTCCACTGCA	2340
CTTTTGTAGG TCGGCTCTAG CAAGGTAGCC TGGTCTATCT TGAAAAATC GCTCCATTTT	2400
TGTACAATCC TATCTTGTCT CATCTCTTGT GTAGAAATTA TCGTATAGCG ACCATTTAAA	2460
CTACGAGATG TATCCTTGAT ATAGGTTTGA AAAGTCATAA GCTGAATAGG TTTGGCTTTT	2520
AGAAAGTCG GAATCOTACC AAGTTTATTG GAAATTTCTT TATTACTATA GACTCCTTCA	2580
CCACTGTGG TAAAATCAAG AGAAGAAATC CCAAACTCTT GGTAGGGGAA GGTATCTTTA	2640
TCAAAAACAC CAGACTTGAC CACCTCATCA CCACTGTCTG TTTTGATGAT GGAGACTTTA	2700
TACTCTTTG ATACATCTCT AAAAAATCGA AGAACAGAGC CTGCAGGTTT GTTAATATCT	2760
TTCAATACA AATCCAAGA ATCTACAGG	2789

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CTCGGAATTT TATTAAGAT AATGTGTTAA TTACAGCGC TCACAACATC TACAGCATG

60

1281

ACTATGGGAA AGAAGCGGAT GATATTTATG TTCTTCCGCG TGITAGTCCA AGTCAAGAAC	120
CAITTTGGAAA GATCAAAGTA AAGGAAGTTC GTTATTTGAA GGAATTTAGA AATTTAAAT	180
CTAAGGATGC AAGGGAATAT GACTTGGCTT TATTAACTCT AGAAGAGCCC ATTTGGTCAA	240
AATTAGGGAC TTGGGTCTT CTTACTAGTC AAAAAATTT GACAGGAATA ACTGTGACTA	300
TCACAGGCTA TCCATCATAT AATTTTAAAA TTCAATCAAT GTATACAGAT AAGAAACAAG	360
TTTTAAGTGA TGATGGCATG TTCTTGGATT ACCAAGTTGA TACTTTAGAG GGGTCTAGTG	420
GATCTACAGT TTATGATGCT AGTCACCGTG TAGTAGGAGT GCATACTTTA GGAGATGGAG	480
CTAATCAAAAT TAACAGTGCA GTTAAATTAA ATGAACGAAA TTTGCCATTT ATTTAACTCG	540
TTCTTAAAGG TACTCTCTT GAAGGATGGA AGAAAAATAA TGGTAGTTGG TACCATTATA	600
GACAAACATGA TAAACAAACG GGTGGCAGG AGATAAATGA TACCTGGTAT TATTTAGACA	660
GTTCGGGTAA GATGCTTACA GATTGGCAAA AAGTCCATGG AAAATGGTAT TATCTCAATT	720
CAATGGGAC AATGGTTACA GTTAGCCAAA CTATCGATGG TAAAGTTTAT AACTTCGCTT	780
CATCTGGTGA GTGGATTAA TGTGGAGGA TATATAAAT GAAGCTTTTG AAAAAAATGA	840
TGCAAACTCG ACTAGCCACA TTTTCTCTCG GTTTGTTAGC GACAAATACA GTATTTCGAG	900
ATGATTCTGA AGGATGGCAG TTGTGTTCAAG AAAATGGTAG AACCTACTAC AAAAAGGGGG	960
ATCTAAAGAA AACCTACTGG AGACTGATAG ATGGGAAGTA CTATTATTTT GATCCTTTAT	1020
CCGGAGAGAT GGTGTGCGC TGGCAATATA TACCTGCTCC ACACAAGGGG GTTACGATTG	1080
GTCTTCTCC AAGAATAGAG ATTGCTCTTA GACCAGATTG GTTTTATTT GTCAAGATG	1140
GTGTATTACA AGAATTTGTT GGCAAGCAAG TTTTAGAAGC AAAAAGTCTC ACGAATACCA	1200
ACAAACATCA TGGGAAGAA TATGATAGCC AAGCAGAGAA ACGAGCTTAT TATTTGAAG	1260
ATCAGCOTAG TTATCATACT TTA AAAAAGTGT GTTGGATTTA TGAAGAGGGT CATGGGTATT	1320
ATTTACAGAA GGATGGTGGC TTGATTTCGC GCATCAACAG ATTGACGGTT GGAGAGCTAG	1380
CACOTGGTGT GGTAAAGAT TACCTCTTTA CGTATGATGA AGAGAAGCTA AAAGCAGCTC	1440
CATGTACTA TCTAAATCCA GCAACTGGCA TTATGCAAA AGGTGTGCAA TATCTAGGTA	1500
ATAGATGGTA CTACCTCCAT TCGTCAGGAG CTATGGCAAC TGGCTGGTAT AAGGAAGGCT	1560
CAACTTGGTA CTATCTAGAT GCTGAAATG GTGATATGAG AACTGGCTGG CAAAACCTTG	1620
GGAACAAAAT GTACTATCTC CGTTCATCAG GAGCTATGGC AACTGGTTGG TATCAGGAAA	1680
GTTCGACTTG GTACTATCTA AATGCAAGTA ATGGAGATAT GAAAACAGGC TGGTTCCAG	1740
TCAATGGTAA CTGGTACTAT GCCTATGATT CAGGTGCTTT AGCTGTAAAT ACCACAGTAG	1800

1282

GTGGTTACTA CTTAACTAT AATGGTGAAT GGGTTAAGTA ATGAAGGCTA APTGTAACCT	1860
GTGATGATA CTTAACTTTG TATAATAGGT GGAATAAAGT CTTCACAATC AAAAAACCA	1920
TAGTATCAAG GTTTTTCTGT ACTGCCCTCA AACAGTTAGA CAATTAATTT ATCOGAAGGA	1980
TTTAGTCTCG TATTGCGACG GCGTAAGTCC TTTTAGTTTT ACCTTAATTC GTTTATTGTT	2040
GTAGTAATCA ATATAGTCTA TAATGGCTTG TTCCAATTGC TTAAGCGACT GAAACGACTT	2100
CTCATAACCG TAAACATTT CCGATTTTCCG AATCCCAAAG AAGGACTCCA TCATACTATT	2160
GTCTGGGCTG TTTCCCTTAC GTGACATGGA TGCTTGAATT CCCTTACTCT CTAGGAACCG	2220
ATGATAAGGA TCGTGTGGT ATTGCCAGCC TTGGTCACTA TGGAGAATCG TATTCTCGTA	2280
GTGCTTCTCT GTGAATGCTT GTTCCAACAT TGTTTGTACT TGTCTAAGT TGGGTGAAGT	2340
TGAAGATTA TAGCGGATAA TTTCGCTATT AAAGCCATCT AAACTGGTG ATAGTAAG	2400
CTTTTGAGTA CTTCCTGGAA TGGCAAATTC TGTCACATCT GTGTGCACT TTTCAATTGT	2460
TTTAGAGCCT TCAAATTGGC CTGAATGAG ATTCG	2495

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 870 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TACCACCGTA TTCATCCAGC AAGATTGCCA TTGTGCTTTG GGTATTTCCG AGTCTCTTTA	60
GCAAGTCATC CACAAAAATA GTTTCAGGTA CAAAAAGTGG ATCTTGTAAG ATTCTCTTCC	120
AAACAATATT GTCAAAACCG TCCACAAAGC CTGCCTTAAG GAGACTCTTG GTGTGAATGA	180
TTCCAAATAC ATTGTCTCTA TCCCATCAT AAACCGGGAT ACGAGAATAA TTTTGTTTTA	240
AAATACTTTG GATAATGGCT TGACTATCAT CCGTAATATC CACCATAAAG GCATCCGTTT	300
GAGGAACCAT AACCTCTCGT GCCATCAGTT CATCGAGCGA AAAGACACCT TGTAGCATCT	360
CAATCTCATC AGCATCCAAT GTTCTTTCAC TATTTGTGCG CATATAGGCA ATTTTCATCC	420
GGGTCACTCT TTCAATCCGA TCATCGAATG ACATAGAGAT CAAATGGCTC AAGAAATTGG	480
TGGAAGCAGC TAAAAAGCAA ACAAAGGAG TGACTAGTTT TCCGATCCCA ATGATAATCG	540
GCGCTGTACG AATTGCCAAG GCATCCTTTA GATTAAGAGC GATTCTCTTA GGATATAATT	600
CCCCAAAAC GATGGAAATA TAGGTCAAAA ATGCCAAGGA TAGAAAAATT GCCACGGCTT	660
GTGCTGTATC GCCATTCCCA AGCCAAAGAG CAATCACACG TCCTAGAGTA TCAGTTAAAC	720

1283

TCGCCCTGA	TAAGATTTGA	ATCAGGGTGA	TTCTTACCTG	GATGGTTGAT	AAAAAGTGT	780
TAGGATTTTC	TAGTACCTTC	AGCAGGCGGA	TGTAGCGTCT	GTCTCTCTCT	TCCGCCTTTT	840
GTTCACACTCG	GGCAGGATTA	AGAGAAACGG				870

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CGTTCGCCAGA	AGCCCCGATT	CTCATCGCCA	ATGTCGTGAT	TGATTTGGCC	CTTTCTCCAA	60
AATCCAACTC	AGCCTATGTA	GCTATGGATA	AGGCACCTGC	TGACCTCAAA	ACATCAGGGC	120
ACTTGCCCTAT	TCCGCGACAC	CTGCGTGATG	GGCACTACAG	TGGAAGCAAG	GAACTGGGGA	180
ATGCCCAAGA	CTATCTCTAT	CCACACAAC	ATCCTGGAAA	TTGGGTCAAG	CAAGACTATC	240
TGCCAGAAAA	AAATTCCTAAT	CATCACTATT	TCCAAGCAGA	AGATACTGGT	AAATATGAAC	300
GGGCTTTTGC	TCAAAGAAAG	GAAGCTATGC	ACGGTTTGGC	AAAAATCTGA	AATCCTTTTC	360
AAAAAAATTGC	ACTTTCTCTCT	TGATTTTTTT	TGAAAAAGTG	GTATCATATA	AATATAGAAA	420
CGCTGTGGTG	TACGACTTCA	CACCTTAAAGT	TTGACCGACT	ATTTTTTGTA	TTATTAGGGA	480
AACAAAAGTC	TTCTAACAGC	ATGTAGGCCG	TCTCACACGG	AAACAGCTTC	AGTTAGAGCG	540
AGTTGCCAC	CTGCTTAATT	GGCGGGGTTT	AATACAAACC	GTGAAGTTTC	GGCACCAATA	600
CAGCTTTTTT	CTTTGCCCTC	TTACCTCAGC	TGGCAGAGCA	GCGGACTCTT	AATCCGTGGG	660
TCACAGGTTT	GATCCCTGTA	GGGGGCATAT	AAATACAACA	GGAAAAGCCT	TATANTATAG	720
GGCTTTTTTT	GCTTTCTCTT	TAAAAAATGT	CGTGCAATTT	CCCGTGTTTT	TACAACAAAC	780
TTTTACAGC	CATAAACTCC	TCACATAATT	TTTCTCCCAA	GGTATGCCCA	TAAACGTCAA	840
TCAACATGGA	GATATCTTTA	TGTCTTAAAA	TTTGGCTCTT	TGTCAACTGT	AGTGGGTTGA	900
AGTCAGCTAA	GCTCGAGAAA	GGACAAATTT	TGTCCTTTCT	TTTTTGATAT	TCAGAGCGAT	960
AAAAATCGT	TTTTTGAAGT	TTTCAAAGTT	CCGAAAACCA	AAGGCATTGC	GCTTGATAAG	1020
TTTGATGAGA	TTATTTGGTG	CTTCCAATTT	GGCGTGTAGAA	TAGTGTAGTT	GAAGGGCGTT	1080
GACGATTTTC	TCTTTGTGCT	TTTAAAGAGT	TTTAAAGACA	GTCGTGAAAA	GAGGAGGAAC	1140
CTCGCTTGA	TTGTCTCAA	TGAGTCGGAA	AAATTTCTCC	GGTGGCTTAT	TCTGAAGTGT	1200

1284

AAACAGCAAG AGTTGATAGA GCTGATAGTG ATGTTTCAAG TCCTG

1245

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

ATGCCTATGT AACTCCACAT ATGACCCATA GCCACTGGAT TAAAAAAGAT AGTTTGTCTG	60
AAGCTGAGAG AGCGGCACCC AGGCTTATGC TAAAGAGAJA GGTTTGACCC CTCCTTCGAC	120
AGACCATCAG GATTACAGAA ATACTGAGGC AAAAGGAGCA GAAGCTATCT ACAACCCGCT	180
GAAAGCAGCT AAGAAGGTGC CACTTGATCG TATGCTTAC AATCTTCAAT ATACTGTAGA	240
AGTCAAAAAC GGTAGTTTAA TCATACCTCA TTATGACCAT TACCATAACA TCAAAATTGA	300
GTGGTTTGAC GAAGCCCTTT ATGAGGCACC TAAGGGGTAT ACTCTTGAGG ATCTTTTGGC	360
GACTGTCAAG TACTATGTGC AACATCCAAA CGAACOTCCG CATTCAGATA ATGGTTTGG	420
TAACGCTAGC GACCATGTTT AAAGAAACAA AATGTGTCAA GCTGATACCA ATCAAACGGA	480
AAUACCAAGC GAGGAGAAAC CTCAGACAGA AAAACCTGAG GAAAGAAACC CTCGAGAGAA	540
GAAACCGCAA AGCGAGAAAC CAGAGTCTCC AAAACCAACA GAGGAACCAAG AAGAATACC	600
AGAGGAATCA GAAGAACCTC AGTTCGAGAC TGAAAGGTTT GAAGAAAC TGAGAGAGGC	660
TGAAGATTTA CTTGGAAAAA TCCAGGATCC AATTATCAAG TCCAATGCCA AAGAGACTCT	720
CACAGGATTA AAAAATAATT TACTATTGG CACCCAGGAC AACAACTACT TTATGGCAGA	780
AGCTGAAAAA CTATTGGCTT TATTAAAGGA GAGTAAGTAA AGGTAGCAGC ATTTCCTAAC	840
TCCTAAAAAC AGGATAGGAG AACGGGAAAA CGAAAAATGA GAGCAGAAATG TGAGTTCTAG	900
TTCTCATTTT TTTCATGAAA ATGTGCAAJA TATAGTAGAT TGAACATAGA ATAGTATACC	960
TCTACTTCTA AAACATTGTT AGAAATCGAT TTGACTGTCC TGTCTCTATT TCATTTTACT	1020
ATATCTTAAC AGATAGTATA AATAAAGATA AACTATTTC TGGCTAATTA ATCAGTTAAA	1080
CACTAGTTAA GGAGTAATCA TGAJAAAAAG AACAACTACT TTATTGATGG CCAGTCTGTT	1140
AGCTCTTGTC TTAGGAGCAT GTGGTTTCTT GGACATATTG ATCCTGGATC ATTCCTCATCA	1200
GGATTACTCT TTACTGCTAT TTTAGAAACT GGGGTGTTTT GATGJAAAGT ATTGCTCTTG	1260
TTATCGTTTC ACATTCCAAA CACATTGCAG AAGGTGTTGT TGAACGTATT AGTAAAGTAG	1320
CTAAGATGTT TCCGATTACT TATGTAAGAG GAACCGAGGG CGGAGGAATT GGAACGAGTT	1380

1285

TTGAACAAGT AGATAGGGTT GTTCCGAAA ATCCAGCAGA TACTTFACTT GCCTTTTTCG	1440
ACCTAGGTTC TGCTAAAATG AACTTAAAAA TGGTGACTGA TTTCAGTGAT AAAAGTATCA	1500
TCATCAACAG GGTTCCAATT GTAGAAGGTG CCTATAATGC AGCTGCTCTT CTTCAGGCTG	1560
GTGCGAACT GTCACTTATT CAAACACAGT TaGCGAGct TGAATCAAT AAATAAGGAA	1620
TTTTCATATA ACTCTTTTAA TAGATAAGCT ATTGATTATC TCAACTATAA TAATGTTAAG	1680
TnAA	1684

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 970 base pairs
 - (B) TYPR: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGGAGTGAG AnATATGAAG ACACAAATTT TCACATTATT GAAAACTGTT GCTGAGATTA	60
TTATTTATTTT GCCATTTTATA ACTAATCTAT AAGTCTTTTA TATTGCTGAA AACCAATTC	120
AAAAAGGCGT ATTAATTGTG GATTTTCTAA TACCTGCAGA GATTGGATAA AGCGTTCAAT	180
CTCTTTTGA TTGCTTCCCT TTGTTTGAAG AAAGACATC ATCTTCTTTA AAAATTTGCCA	240
CGATACTTTT TCAAAAACAT CATACGCTCG TAACATCCTC TCCAACCTCG CTTCGAAGAT	300
TGGAGTGAG GAGAAAAATT TTCGCTCCAT GAGTCTGAT AAGATATTTA AGAGTCTCTG	360
CTTCATATAC AATCGATTGT GTACTAATCT TTTAAATTTT TTGGATTTT CGAGTAAGGA	420
GGTTGATAAA AAAATCAGAT CTTGATTGCT CAAGAAGGGC ATGTTATTGC AAAAGAGATA	480
GAGTTCAAC CAGGTCCAAG ACTCGATAGC ATAGAGATAG GTGGTCAAAA ACTGCTATC	540
CTCTCTGCT ACTGGGTAGC TTTTATTTAG TGAATGGATG GCATCTTTAA TCACGATGCG	600
ATTCAAAACA CGATAGGTCT GCGCCATCTG TTCTTGATCG ACTTCTTCCA ATAGTGCCTC	660
TAAAGCAGCT ATATCTTGAT GGGCAAAGCG ATTCACAACC TTTTCGACCGA TTCCGATATG	720
TGGAGATTCT TGATAGTTGT TGAGCTTGCG CCCAAACTCA TCAAAAGTCA CATTTATACC	780
TTGATATAGT AGAATCAACT TATCCGACAGA CAGCATAGAC TGCCCTAGTT CAAACTTGA	840
CAACTGAGAA GCTGTTAGAC CCTCACAAGC CACATCTGAC TGCTTGAGCT TTCTGCGCAA	900
ACGTAAATTC TTGTAAAAAT CCCCCAGTTC CATTTCTCTCA ATCATCTGAC CACCTCCTAG	960
CTTTTGCAGG	970

1286

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2996 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GTGTGACCACG GGTAAACTA CCTAACTGC AGCTATCACA ACTGTTTGG CACGTCGGTT	60
GCCTTCATCA GTTAACCAAC CTAAAGACTA TGCCTCTATC GATGCTGCTC CAGAAGAACG	120
CGAAGCGCGT ATCACTATCA ACACTGCGCA CGTTGAGTAC GAAACTGAAA AACGTCACCTA	180
CGCTCACATC GACGCTCCAG GACACCCGGA CTACGTTAAA AACATGATCA CTGGTGCTGC	240
TCAAAATGGAC GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CACAACTCG	300
TGAGCAGATC CTTCCTTACG GTCAGGTTGG TGTTAACAC CTATCTGCTT TCATGAACAA	360
AGTTGACTTG GTTGACGACG AAGAATTGCT TGAATTGGTT GAAATGGAAA TCCGTGACCT	420
ATTGTACGAA TACGACTTCC CAGGTGACGA TCTTCCAGTT ATCCAAGGTT CAGCACTTAA	480
AGCTCTTGAA GGTGACTCTA AATACGAAGA CATCGTTATG GAATGTATGA ACACAGTTGA	540
TGAGTATATC CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTCGAGGA	600
CGTATTCCTA ATCACTGGAC GTGGTACAGT TGCTTCAGGA CGTATCGACC GTGGTATCGT	660
TAAAGTCAAC GACGAATTCG AAATCGTTGG TATCAAAGAA GAAACTCAAA AAGCAGTTGT	720
TACTGGTGTT GAAATGTTCG GTAAACAACT TGACGAAGGT CTTGCTGGAG ATAACGTAGG	780
TGTCCTTCTT CGTGGTCTTC AACGTGATGA AATCGAAGT GGACAACTTA TCGCTAAACC	840
AGGTTCAATC AACCACACA CTAAATTCAA AGGTGAAGTC TACATCCTTA CTAAAGAAGA	900
AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA CAATTCTACT TCCGTACTAC	960
TGACGTATACA GGTTCAAATC AACTTCCAGC AGGTACTGAA ATGGTAATGC CTGGTGATAA	1020
CGTGACAATC GAOGTTGAGT TGATTACCCC AATCGCCGTA GAACAAGGTA CTACATTTCTC	1080
TATCCGTGAG GGTGACGCTA CTGTTGGTTC AGGTATGGTT ACAGAAATCG AAGCTTAATT	1140
CGATTTAGTT CCCAGAAGAA CAATTATTTA AGTTAGACAC TAAAGAAGTC TTGCTTGCCA	1200
AGGTTCTTTT TTTAGATATT GAACTAATAC TCAATGAJAA TCAAAGAGCA AACTATAATA	1260
TATTGAAACT AGAATAGTAC ACATCTACTT CTAJAAACATT GTTAGAATC GATTTGACTG	1320
TCCTGATCGA TTTGTCTTGT TCTTATTTCA TTTTACTATA GAAAGTTAGC TACAGACTGC	1380
TCAJAACATT GTTTTTAGOT TGTAGATAGA ACTGACGAG TCAGTAACAT CTATACGACA	1440

1287

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AGGCGAAGCT GACGCGGTT GAAGAGATT TCGAAGAGTA TAATACTAGA CTAAAAACAA 1500
AAAGCATTAT ACAATAGTAA TATGAATCA ATTAAGAAG AATCCAAAC CATCAAAACA 1560
CTTTTAAAG ACTCTCGTAC AGCTAAATAT CATAAACGCC TTCAAATCGT TCTATTTCTGT 1620
CTGATGGGCA AATCTTATTA AGAGATTATA GAACITTTAT AGTGGTTGA AATAAGATGT 1680
GAACAACCTC ATCAGGAAAG TCAAACATAT TTATAGAAAT ATTTAGCAG CCAAGGTGTA 1740
CTGTTATAGA TTCAATACAC TTTAGACTGT AATCAAAACA CGATTGGCG AAATGTAAAA 1800
AATATGAGGA GTTCGACTC GACTCTCTCC TTCAGAAAC ACGTGGTGGT CGTAACCATG 1860
CTTATATGAC GGTGAGCAA GAGAAAGTCT TTCTGCCCC CCATTGGAAG GCTACAGAGG 1920
CAGGAGAAAT TGTACAAAT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG TTAGGTCCTT 1980
CCTACACAGC TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA AATATTCAGC 2040
CAGTCCAGA ACATCCTAAG AAGCAGATG CTCAAACCAT TGTGCGCTCT AAAAATAAAG 2100
TCTCAATTCA AGAAGACAAG TGAATGCAC CCCAAAGTT AGACAGAAA AATCTAACTT 2160
TTGGGTGTT TTTATTATGA AATTAACTTA TGATGATAAA GTTCAGATCT ATGAACATTG 2220
AAAACAAGGA TATAGCTTAG AGAAGCTTTC AATAAATTT GGGATAACA ATTCTAATCT 2280
TAGGTACAGT ATTAAATGA TTGATCGTTA CGGAATAGAG TTCGTCAAAA AAGGAAAAAA 2340
TCGTTACTAT TCTCCTGATT TAAAAAAGA AATGATTCT AATCTCTGAC ATGAAGGCTG 2400
GACTAAAGAT AGAGTTTCTC TTGAATACTG TCTCCCAAGT CGTACGATAC TTCTTAACTG 2460
GCTAGCAACA TACAGGAAAA ACGGTATAC TATTGTTGAG AAAACAAGAG GGAGAGTACC 2520
TGAGAGCGGA GAATGCCATC CTAAAAAAGT TAAGAGAAT CCGATTGAAG GAGGAAAAAG 2580
AGAAAGAGA AAGACAGAAA TTATTCAAGA ATTAATGACT GAGTTTTCTG TAGATATTCT 2640
TCTAAAGGCC ATTAACCTAG CTCGTTTGAC CTACTACTAT CACTTGAAC AGCTAGATAA 2700
ACCAGATAAG GACCAAGAGC TTAAGCTGA AATTCAATCC ATTTTATCG AACACAAGGG 2760
AAATTATGCT TATCGTCGGA TTATTATTAGA ACTAAGAAAT CGTGGTTATC TGTAAATCA 2820
TAAAGAGTGT CAAGGCTTGA TAAAGTACT CAATTACAA GCTAAAATGC GACAGAAAGC 2880
AAATATTCT TCTCATAAAG GAGACGTTG CAAGAAGGCA GAGAACTCA TTCAGGACA 2940
ATTTGAAGGC TCTAAACAA TGGAAAGTG CTACACAGAT GTGACAGAA TTGCGC 2996

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(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 837 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

1288

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

CTTATCAACT CCCGACATGG CTCTCAGACC AATCCAAATC CCTAAAAAA TCAGAACAAAG	60
GATGGTGGTC AAGATCAAAC TCTCGAAATA TAAAGAAATC AGTTCCAGTA GCATGATTC	120
TCTCATTTCT ATCTTTTTTA AAGAGTAAAC TCAGCTAGTC CAACTAACTG AGTTTCCTT	180
TATCTATTAT ATCAATATA AGTCCGTTTG TAACTAGCGA AGAATTCCTT TGTCCGCTCT	240
TCTTTAGGGG TGTGGATAAT CTCTCCGGA GTTCCAGACT CGATGATTTT CCCCTTATCT	300
AAGAAGAGAA TTTTATCCGC AACTTGGGCT ACAAGGACA TGTGATGACT GACCAAAATC	360
ATGGTCTGAC CTGACTAGC AGCATCTGCA ATAGACTTTT CTACTTCACC GACCAATTCT	420
GGGTCAAGGG CTGAAGTTGG TTCGTCTAAG AGCAAAACAT CTGGTTTCAT AGCAAGCGCA	480
CGCGTAGGG CAACCCGTTG CTTCGTGCCA CCTGATAAAT GCGAGGATA ATGOTTTC	540
CGGTGCGAAA GCCCAACCTT AGCCAATCT TCCTTGGCAA TCTTAGTCGC TTCTTGCTCA	600
GATAATTTCT TGACAACAAC CAAGCCTTCT TTCACATAT CAAGTGCTGT TCGGCGTCA	660
AACAAATTA ACTGPTOGAA AACCATAGAC AACTTACGAC GTAGGGCAAG GATTTCCTCT	720
TGAGTGATTT TAGAAAAATC AACTGAAAAA CCATCAATCT GAATAGAGCC ACTGTCAGGT	780
GTTTCTAGAT AATTGAGACT GCGAGAAAG TTCAATTTCA GCTCTGAAGA CCAATCA	837

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 868 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CCGAACAAAA TGGGCTAATT AGATTATAGT AAGAAAGTA AGTTAAAAAT GAGAATTGCA	60
ATTGGATGTG ACCACATCGT AACTGATGAA AAAATGCGCG TTTCAGAAAT TTTGAAATCA	120
AAAGGATATG AAGTCATTGA CTTTGGTACC TATGACCATA CACGGACTCA CTACCCAAATC	180
TTTGGTAAAA AAGTAGGGGA AGCTGTAAC AGCGGTCAAG CTGATCTTGG AGTATGTATC	240
TGTGGTACTG GTGTTGGTAT CAACAACGCT GTAAATAAAG TTCCAGGTGT TCGTTCTGCC	300
TTGGTTCGTG ATATGACAAC AGCCCTTTAT GCTAAGAAGC AATTGAACGC TAACGTTATT	360
GCTTTTCGTG GTAAAAATAC TGGTGAATTG CTTATGTGTG ATATCATCGA AGCTTTCATC	420

1289

CATGCTGAAT	ACAAACCAAC	TGAAGAAAAC	AAAAAATTGA	TTGCGAAAAAT	TGAACATGTT	480
GAAAGTCACA	ATGCTCAACA	AACAGACCCA	AATCTCTTTA	CAGAATTCCT	TGAGAAATGG	540
GATCGTGGAG	AATACCAAGA	CTAAGAGGTG	ACCTATGATT	TTAACAGTCA	CAATGAACCC	600
ATCCATCGAT	ATTTCCATATC	CCTTGGATGA	GTTGAAGATT	GATACTGTCA	ATCCTCTGGT	660
GGATGTAAAC	AAAACGGCTG	GTGTAAGGG	ACTCAATGTT	ACCCGAGTAC	TTTCAGAAAT	720
TGGCGATTCT	GTCTCTGCTA	CTGGTTAGT	GGGTGCAAAA	CTTGGTGAGT	TTTTCGTTGA	780
ACATATCGAT	AATCAAGTAA	AGAAAGATTT	CTTCTCAATT	AAGGGAGAAA	CTCGTAACGT	840
TATCGCTATT	CTCCACGGAG	ACAACCAA				868

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3744 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CGGTCAAAAG	TCTTCATAAG	ACTCGAAAGT	CACAGTTCTT	TCGTTCTTGC	TGGCATCTAT	60
ATAGGTAATT	TCAATCATGT	TTAAAACCTC	TTTGTTTAAT	GCTAACTTTA	TTTACTCTCT	120
TATAAAAGAG	AATGTCAAGA	AAAATGATTG	CGCACGCAAC	TTTTTTTAAA	ATCATCTTAA	180
ATCAAGAAAT	CCAAACCTGC	TTCCAAGCTT	TCTTCGACAG	TCTTTTGTAG	CGAGGCCAGT	240
GTCTTTTGGC	CATCATTTGT	CAGCGAGATA	AAACTAGAGC	GTCTATCTTG	ATGCAACAC	300
ATCGCAGTGA	GTAGACCGCA	ATTTTATAGT	TCCAAGCGAG	CCACCATCCT	AGAAACTGCG	360
CTCGCGCTCA	GATGAAGCTT	ATCTGCGAGG	TCAATCTGGC	GTAGAGATTT	TTCTTCAGCC	420
AAGTCCAGAT	AGTAGAGCAG	GTAGAAGCTT	TTCAAGGTCA	GACTTTGCTC	CTCTGTGTGG	480
GCAATGGTCT	CTTCCAAGAG	ACTTTCAATT	TCTTTCTGAC	GCCGATTGAA	GTCAAACCAT	540
TTTTCCAAT	AGGTTCATAGT	GTCTCTTTTC	TTTTTATAGT	CATAAATAGA	AGAAAGTCCA	600
TTAACGGCCA	GTCTCTGCGT	CACAAGATGA	TTGCGCATGC	AATAATTATA	CTACTTTTCA	660
AGAATGCTGG	CAAGCTCTGT	TTTTTATGGG	TTTATTTTAT	GTGTGAATAA	TGGGGGAATC	720
CTATTGTTTC	AATTTCTAAC	TCCTTATCAC	ATTCGAATTC	AGATTTTATT	TCATTTCTCT	780
ATCTATAGTT	GCTTATGTTA	AAATAAGCAT	GCTCTAATAA	AGCTATGCAT	ATAGTACTGA	840
TTTTAAACAA	CGAGCAATTAG	ATTCCATTAA	AGGAGGGCAC	AGACATGTCG	AGCGCGCCAA	900

1290

AGTTTTTCAT	GTGCGGTCA	GAACCTCTCT	CACGTGGGAA	AAGAAAGACG	TAAACAAGGG	960
AACCTAGAGC	GGAAAAAGCG	AGTCGTCAAA	AAGCGTAAGA	TCCCTTTTGA	AGAATTGAAA	1020
GCCTTTGTAG	AGGCTCATCC	AGACGCTTTT	TTAAGGGAAA	TTGCGGCCCG	TTTGTATTGT	1080
GCTTTGCCCT	CCGTATGGG	AGTTTAAAG	CAGATTAAAG	TCATTTTAAA	AAGACGACC	1140
AGTTTTAGGG	AACAAGAGCC	TGAGAAAGTT	CTCGAGTTC	TTGATATTTT	GGATACCTTA	1200
AAAGATTTAC	CAGTCCTATA	TATTGACGAA	ACGGGAATCG	ACCGCTACCT	CTATCGTCT	1260
TATGACGGGG	CTCCTAGAGG	GGAGAAAGTC	TATGGCAAGA	TTAGCGGACG	CGCTTTTGAG	1320
CGACTAATG	AGGTGGAGCA	AAAACCTCAAT	GGTAGTTTTC	TAATCAGATA	TATTGATTCA	1380
CAAAATTAGAG	AATGAAAGAA	TAATTATGCA	TAAAAATAGG	AATATAAACCC	AAAAAATTAGC	1440
TGATTTATAC	TCATTTGCGT	GTCTTTATAA	AAAACCTTATC	TTATAATATA	TATATATATA	1500
TATACAAAAT	AGTAAAATGC	TTTTTTTTTT	TAGCAAAAAT	ACCTCAAGTT	TCTTGCTATT	1560
TTGGTTTCCC	TATTCATAAA	TTATAGTATG	GTAATTATTT	TATATCCATA	CATGAAAAAT	1620
ATACTCGAAA	GGAAATTTC	AAATATTTTT	TAGACGTCAG	AAGGTTGAAT	ATAGAGAAAC	1680
AGACCGAGTA	ACTCGGTTC	AATTAAATCA	ATCAGGGAAG	CATTGGCTAC	GGGCTCGAC	1740
TTCTCTTTTT	GGCTTGTTTA	AGGTCTTGCG	AGGTGGTGT	GATACTACTC	AGGTCAATGAC	1800
CGAAACGGTA	GAGATAAAG	TAAGTCATTC	AATTACTGGG	CTTGATATCC	TCAAGGGGAT	1860
AGTGTCTGCG	GGAGCTGTCA	TAAGTGGAAC	CGTGCACACT	CAAAACGAAGG	TATTTACAAA	1920
TGAGTCAGCA	GTACTTGAAA	AAACTGTAGA	GAAAACGGAT	GCTTTGGCAA	CAATGATAC	1980
AGTAGTTCTA	GGTAOGATAT	CTACAAAGTAA	TTACAGCGAGT	TCAACTAGTT	TGTCAGCTTC	2040
AGAGTCGGCA	AGTACATCTG	CATCTGAGTC	AGCCTCAACC	AGCGCTTCGA	CCTCAGCAAG	2100
TACAAAGTCA	TCAGAAATCAG	CAAGTACATC	GGCTTCGACA	AGTATTTCTG	CATCATCTAC	2160
TGTGATAGGT	TCACAAACAG	CTGCCGCTAC	AGAAGCAACT	GCTAAGAAGG	TGGAAGAAGA	2220
TCGTAGAAAA	CCAGCTAGTG	ATPATGTAGC	ATCAGTTTACA	AATGTCAATC	TCCAATCTTA	2280
TGCTAAGCGA	CGCAAGCGTT	CAGTGGATTTC	CATCGAGCAA	TGTGCTGGCT	CTATAAAAAA	2340
TGCTGCTGTT	TTTTCTGGCA	ATACGATTGT	AAATGGCGCC	CCTGCAATTA	ATGCAAGTCT	2400
AAACATTTCT	AAAAGTGAGA	CAAAAGTTTA	TACAGGTGAA	GGTGTAGATT	CGGTATATCG	2460
TGTTCCAATT	TACTATAAAT	TGAAAGTGAC	AAATGATGGT	TCAAAATTGA	CCTTTACCTA	2520
TACGGTTAGC	TATGTGAATC	CTAAAACAAA	TGATCTTGGT	AATATATCAA	GTATGCGTCC	2580
TGGATATTCT	ATCTATAAAT	CAGGTACTTC	AACACAAACA	ATGTTAACCC	TTGGCAGTGA	2640
TCTTGGTAAA	CCCTCAGGTG	TTAAGAAGTA	CATTACTGAC	AAAAATGGTA	GACAGGTCT	2700

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ATCCTATAAT ACATCTACAA TGACGACGCA GGGTAGTGGG TATACTTGGG GAAATGTTGC	2760
CCAAATGAAT GGTTCCTTTC CTAAGAAAGG ATATGGATTA ACATCATCTT GGACTGTACC	2820
AATTTACTGGA ACGGATACAT CCTTTACATT TACCCCTTAC GCTGCTAGAA CAGATAGAAT	2880
TGGAATTAAC TACTTCAATG GTGGAGGAAA GGTAGTTGAA TCTAGCAAGA CCAGTCAGTC	2940
ACTTTTCAGAG TCTAAGTCAC TCTCAGTAAG TGCTAGTCAA AGCGCCTCAG CTTCAGCATC	3000
AACAAGTCGG TCGGCTTCAG CATCAACCAG TGCTCGGCTC TCAGCCTCAA CCAGTCGCTC	3060
AGCTTCAGCA AGTACCAGTG CTTCAGTCTC AGCATCAACA AGTGCTTCAG CCTCAGCATC	3120
GACAAAGTCCC TCGGCTTCAG CAAGCACATC AGCATCTGAA TCAGCCTCAA CCAGTCGCTC	3180
GGCTTCAGCA AGTACCAGTG CTTCAGCTTC AGCATCAACC AGCGCCTCGG CCTCAGCAAG	3240
CACCTCAGCT TCTGAATCGG CCTCAACCAG CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC	3300
TGAATCGGCC TCAACCAGCG CCTCAGCCTC AGCATCAACA AGTGCTTCGG CTTCAGCAAG	3360
CACAAGCGCC TCGGCTTCAG CATCAACGAG TACGTGAGCT TCAGCCTCAA CCAGTCGCTC	3420
AGCCTCAGCA TCAACAAGTG CGTCAGCTCA GCAAGTATCT CAGCCTCTGA ATCGGCATCA	3480
ACGATGCGGT CTGAGTCAGC ATCAACGAGT ACGTCAGCCT CAGCAAGCAC CTCAGCTTCT	3540
GAATCGGCC CTCAACCAGTG GTCACTCAG CATCGACAAG CGCCTCAGCT TCAGCAAGTA	3600
CCAGTCGCTC AGCCTCAGCG TCGACAAGTG CGTCGCGCTC AACCACTGCA TCTGAATCGG	3660
CATCAACCAG TGCGCTCAGCC TCAGCAAGTA CTAGTGATTC GGCTTCAGCA TCAACCAGTG	3720
CCTCGGCTTC AGCCTCAAC AGTG	3744

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CGATAAAGAG GCCTTGAGTA ATCTCAATT GCAGATTGAA AATGGAGAGA TTATGGGCTT	60
GATTGTGTCAT AATGGGGCTG GAAATCGAC CACTATAAAA TCCCTAGTCA GTATCATTTT	120
ACCCAGCAGT GGTCTATTTT TGGTAGACGG TCAGAGTTTA TCGGAAAAAT GCTTGCTAT	180
TAAACGAAG ATTGGCTACG TAGCAGACTC GCTGACTTAA TTTTACGCT TAACGGCCAA	240
TGAATTTTGG GAATTGATCG CCTCATCCTA TGATCTGAGT AGATCTGACT TGGAGGCTAG	300

1292

TCCTAGCTAGG CTATTGAACG TTTTGGATT	TCGTGAAAAT CGCTATCAGG TTATTGAAAC	360
TCCTTCTCAC GGAAATGCTC AGAAAGTCTT	TGTCATCGGA GCACCTCTGT CTGATCCCGA	420
TATTTGGGTC TTGGATGAAC CCTTGACTGG	TTTGGATCCC CAGGCTGCCT TTGATTTGAA	480
ACAGATGATG AAGGAACATG CACAAAAGG	GAAGACAGTC TTGTATTCAA CTCATGTCTT	540
AGAGGTGCGA GACCAAGTCT GTGATCGGAT	TGCTCATTTG AAAAAGGGGC ATTTGATTTA	600
TTGTGGTAGT GTAGAGGACT TGAGAAAAGA	TTACCCAGAC CAGTCTTTGG AAAGTATCTA	660
CCTTAGTCTT GCTGGTAGAA AAGAGGAGGT	TGCGGATGCG TCTCAAGGTC ATTAATAAAT	720
TAGTTGATAT CAATATCCTT TATTCAATCT	AAGAAGCTAA TCTGCCTAAT CTACGAAGA	780
AGCAGGCTAA GAATC		795

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTAATGTG CTTGGCAGCG TCCCTGACAC	TGCTACTACC ATTTCCCATTA GCGACCGACA	60
TACCAACGCC AGCCAGCATT TCAAGATCAT	TATCTGAGTC ACCAAAAGCC ATGACTTTGT	120
TGAGGTCAAA GCCATATCTT TTCCCAACTC	GCGGAATGCC TTCTAAATTTA GAAATTCCTT	180
GATTGATGAC ATCCGATGCA AAGGATTGCT	TACGTGTCAA TTTCGAAGTCT TCAAAATCAG	240
CTGCCGCCTT CTCAGATTCT TCTGGTGTCA	TCAGCATCAA AACTTGGTAG ATAGGCTGAT	300
TCATCAGGTG AAGCAGGTCC TCTTCTTTT	GCGGAACAC CTTGCTGACC ATGCCATTAA	360
AAGACTGACT CACCCTCCGA GTTAAACAG	AGGGAACGAA GCGACTAATT CGTTGGGAAA	420
AAGAACCAG ACCAAAGAC ATGATTTTAG	AACCAACAT GGCATCCTTG GTCCCTAGAG	480
CAATCTCCGT GCCCTCTTTT TTAGCATAGC	TAAATTAGAT GCGCAATGT AACTTGGAAA	540
TAGGGCTGCT GAACAAGACT CTGTCTTTAC	TAAAGATATA CTGGCCATTA TAGGTACCG	600
CAAAATCCAG ATCCAAATCG TCCATCAATT	CTTAAACAAA AAAAGGTCTT CGCCCTGTCC	660
CTACGCCAAC TAGTACCCCT TGTCTCTTGA	CAATCTTAAT CGCATCCTTA GTGGATTCTA	720
AAACACTCTT GCGATGTGTT ACCAAGCTC	CATCGATATC AAAAAAACA GCTTTGACTT	780
CCATCTATTC CCAATCTCCC CTTTGTGAT	ACAAATGATTA TACCACATCT CAGAAAGAGT	840
GAGTAAATCA TGCTTAAGA AATCCTTGTT	TTACATACGG GTGGAACATP TTCCATGCAG	900

1293

GCCGATGCTT CTGGCGCTGT TGTGACGAGT TCAGATAATC CCATGAACCA TGTGTCCAAC 960
 CCACCTGAAG GAATCCAAGT CCACGCGCTT GACTTTTTTA ACCTTCCAAG TCCCATATATC 1020
 AAACCCAAAC ATATGCTGGT CCTCTACCAG AAAATTAAAG AGGAAGCAGA TAACTACGAT 1080
 GGAGTGGTGA TCACACACGG AACCGATACT TTAGAGGAAA CAGCGTATTT CTTGATACC 1140
 ATGGAAGTTC CCCATATGCC TATCGTTCTA ACAGGAGCCA TGGGTACTCC AATGAGCTCG 1200
 GTAGTGATGG TGTTTATAAT TACCTAAGTG CTTTACGAGT GGCCAGCGAT GACAGGCGTG 1260
 CTGACAAAGG AGTTTTGGTC GTTATGAACG ATGAAATCCA CGCTGCCAAG TATGTCACCA 1320
 AAACACATAC GACTAATGTC AGCACCTTCC AGACTCCAAC ACATGGCCCC CTGGTCTCA 1380
 TCATGAACA GGAATCTCT TACTTCRAAA CAGCTGAACC TCGTGTTCGC TTTGACCTTG 1440
 ATCAGATACA AGGTTTAGTC CCTATCATCT CGGCTTATGC TGGTATGACA GATGAGCTGA 1500
 TTGATATGCT GGATTAGAA CACTTGGACG GTTTGATTAT CCAAGCCTTC GGAGCTGGTA 1560
 ATATTCCCAA AGAACGGCT CAAAATTAG AAGGCTTCT GCAAAAAGGA ATTCCAGTCG 1620
 CTCGTGTATC ACGATGCTTT AACGGTATTG CCGAGCCTGT TTATGCATAC CAOGTGGGG 1680
 CGGTACAGTT GCAAAAAGCA GCGTTTTTCT TTGTTAAAGA ACTCAACGCC CAAAAGCTC 1740
 GCTTGAJAAT CCTCATGCC CTCAATGCCG GACTAACAGS ACAGGCTTTG AAAGACTATA 1800
 TGGAAAGCTA ATACTCTTCG AAAATCTCTG CAAACCAAGT CACGTGCGCT TACCGTATGT 1860
 ATGGAECTGA CTTCGTCAAT TTCATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG 1920
 TCAGTTCTAT CTACAACCTC AAAACATGT TTTGAGCTGA CTTCGTCAAT TCTATCTACA 1980
 ACCTCAAAAA CATGTTTTGA GCTGACTTCG TCAGTTCTAT CTACAACCTC AAAACATGT 2040
 TTTGAGCTGA CTTCGTCAAT TCTATCTACA ACCTCAAAAA CATGTTTTGA GCTGACTTCG 2100
 TCAGTTCTAT CTACAACCTC AAAACATGT TTTGAGCTGA CTTCGTCAAT TCTATCTACA 2160
 ACCTCAAAAA CATGTTTTGA GCTGACTTCG TTAGTTTCAT CTACAACCTC AAAACATGT 2220
 TTTGAGCTGA C 2231

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1310 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

1294

GAGTCAAAGG CTCCGAGGTT GACTTTTTAC AAGGGGACAG GTGAATATTA TCTAGACCTG	60
TCAGAAATTC TCTTTCTTGA AACAGAAAGG AGCAAGATCT ACCCTCATAA CCAGAAGGAA	120
GCTTATGAGG TTCGCCTCAA GCTCTATGAG TTGGAGTCTA TCTTGCTCG CTATTTTAAT	180
CGAGTTTCCA AGTCAACGAT CGCAACATC CGTCAGATTT ACTCAGTGA CAAGTCCTTT	240
TCAGGAACGG GCACCATTC CTTTATCAG AGCACAAGG AGGTTCATGT CTCACGGCAT	300
TACCAATCCC TCCTAAAGA AATCTAAGA AACATGAGGT AAAAAACATG AAAAAAGAAAG	360
CATTGCTAT TGTTTTATG GTTTTACAG CTTGGATCTT GCTGCAAGG AATTTGGAA	420
TTCTCTCTTT GGATGGTAAA ATATGGCCTT TACTAGGTAT TGTTTTTTTT GCTTATAAGT	480
CCATTGAGTC CATCTTAGA CGTCATCTCA CTTCGGCAGT TTTTACAGST TTACTGGCGC	540
TCATCATTCG AAATTACGCT TATGACTTGT TACCAGTTAC CAATCATCT CTATTTTGGG	600
CTAGCATCTT GGTGGTACTT GGTGTTGGTT ATCTGACGCA TTCAGTAAAG TTCTGGAATG	660
AAAAAAATG GTGTACAAT GGGAAAAAAG CAGTCGTAC AGATAGGAA GTGCTTTTGG	720
GTAGCGGGAC CTCTATAAG CAAGATCAG ATCTGTAGA TGACCAAGTG GAAGTCGCTT	780
TTGGGGATGC TAAATCTAC TATGATAATG CAGAGATGCT AGGTGATTTT GCAACTTTAA	840
ATATTGAAGT GCCCTCGGG AATGCAACCG TCTATGTTCC ACAACACTGG CGGTAGATT	900
TGAAAGTAGA AACCTCCTTT GGTGCAGCTA AGGCTGACGC TCTGTAGCC CCAACCAGCA	960
AAACCTTGAT TATCGGTGA GATGTGGCTT TTGGGAAGTT GGAATTTGTC TACGTTAAAT	1020
AAAAAATCT TCACCTCAAC CATCAAATA GACGTACTAA GAATAGGAAA TTGATGCCCT	1080
GCTCTGATTT CAGTTCTATG GTTGTTAGAC TTTAAAAAAT GAAATGCTGC CTTTAAAGT	1140
TGTATATTTT TCGATATTTT GCCTTTTACG TTTGATGAT CTATGTACTA CAGCGTAGAT	1200
GATGTAGTGT CAAATGCTTT TAAAAACGG ATGATATTGG ACAGTTTTT TGCCTTTAAT	1260
TGCTCAGGAA CATGAAGT CAGTACCTGG GTTTATGACA AGGAGAAATG	1310

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

ACTCTGATTT GATTGGAAC ACAGTCGGTG CCATTGCAGT TACTTCAAC GTAACGACTT	60
ATCTTGAGTC TGCTGCTGGT ATCGGTGAG GTGGACGTAC TGTGTTGACA GCCTTGCTTG	120

1295

TAGCTATCTG TTTTGGGATT TCAAGCTTCT TTAGCCCACT TCTAGCGATC GTACCAACAG 180
 CGGCTACAGC TCCAATCTTG ATTATCGTTG GGATPATGAT GCTTGGTAGC TTGAAAAATA 240
 TCCATTGGGA TGATATGTCT GAAGCAGTTC CTGCCCTCTT CACATCTATC TTTATGGGAT 300
 TCAGCTACTC TATCACTCAA GGGATTGCAG TTGGTTCTCT GACTTTACACT TTGACTAAGC 360
 TTGTTAAAGG TCAAGTTAAA GATGTTCATG TCATGATTTG GATTTTGGAT GCCTTGTTTA 420
 TCCTTAAC7A CATCAGCATG GCCTTATAAT AGAATGACCC AGGGGGATTT CCCCCCTTTT 480
 TTAATACaG CAGATAGGTG ATGAAAGAGA AAAATATGTG GAAAGAATTG TTGAATCGTG 540
 CAGGCTGGAT TTTGGTCTTT TTACTTGCCG TCCCTTTATA TCAGGTTCCT CTAGTGGTTA 600
 CCTCTATTTT GACTTTAAAA GAAGTAGCCC TGCTACAGTC AGGGCTGATA GTTGTGCGCC 660
 TTTCAATTGT GGTTCGTGGT CTATTTATTA TGGGAGCTCG TAAACCAAG TTAGCTAGTT 720
 TTAA7TTTTC TTTT7TTAGA GCTAAAGATT TGGCAGTTT GGCTTTGAGT TATCTAGTTA 780
 TTGTCCGGTC AAATATCTT GGTTCATTT TATTGCAACT GTCAAAATGAG ACGACAACAG 840
 CTAACCAATC TCAGATTAA7 GATATGGTTC AAAATAGTTC GTTGATTTCC AGTTTCTCTC 900
 TGCTAGCCCT GCTTGCTCCG ATTTGTGAGG AAATCTGTG TCGTGGGATT GTTCTTAAAA 960
 AGATTTTCCG AGGCAAGGAG AACCTGGGAT TTGTAGTCGG TACGATGTG TTTGCTTTAT 1020
 TGCA7CAACC AAGTAATTTA CCTTCTTTAT TGATTTATGG AGGTATGTGC ACAGTTCTAT 1080
 CTTGGACAGC CTACAAGACC CAACGTTTGG AAATGTGAT CTTGCTTCAC ATGATTTGTTA 1140
 ATGGGATTCG TTTCTGTTTG TTGGCTCTTG TGGTGATTAT GAGTCGGACA TTAGGAATTT 1200
 CTGTTTAAAA GTTTTATGTT AGGAACCGAC CTC7TTCTAC CAGGGAAAAG TGAATGCAAT 1260
 CGTGCCATC TTTTCTCTTT TATGTTAAAA TAGAAAAATA ATATGATGAA AATCCTTGAG 1320
 GGAGTGACCG ATATGTCaAG TAAAGCCAAT CATGCAAGA CAGTTATTTG CGGAATTA7C 1380
 AATGTAACCC CAGACTCCTT TTCCGACGGT GGTCAATTTT TTGCTCTTGA GCAGCGCTC 1440
 CAGCAGGCTC GTAAATTGAT AGCAGAAGGA GCCAGTATGC TAGATATCGG CGGAGAA7CG 1500
 ACTCGGCCGG GAAGTAGCTA TGT7TGAGATA GAAGAGGAAA TCCAGCGTGT TGT7CCAGTG 1560
 ATCAAA7CGA TTCCGAAGGA AAGTGATGTC CTCATCTCTA TTGATACTTG GAAGAGTCAA 1620
 GTAGCAGAGG CTGCTTTGGC TGCTGGTGCC GATCTAGTCA ATGATATCAC TGGTCTTATG 1680
 GGTGATGAGA AAATGGCTTA TGTGGTAGCT GAAGCGAGAG CGAAAGTGGT CATCATGTTT 1740
 AACCAGTTA TCGCTCGACC TCAGCATCTC AGTTGCGCTA TCTTCCCTCA TTTTGGTTT7 1800
 GGTCAACCT TTACAGAAA AGAGTTAGCT GACTTTGAAA CATTTGCCAT CGAAGACTTG 1860

1296

ATGGTGGCTT TCTTTGAACG AGCACTAGCG AGAGCGGCAG AAGCTGGTAT TGCACCAGAA	1920
AATATCTCTGT TGGATCCAGG AATTGGCTTT GGTCTGACCA AGAAGAAAA TCTGCTTCTT	1980
TTACGCCACC TGGATAAAT ACATCAGAAG GGCTATCCAA TCTTTCTCGG AGTGTGCGGC	2040
AAGCGATTG TCATCAATAT CTTAGAGGAG AATGGTTTTG AAGTCAATCC TGAGACAGAG	2100
CTTGGTTTCC GAAATCGGGA CACGGCTTCG GCTCATGTAA CTAGTATCGC TCGGAGACAG	2160
GGTGTAGAAG TGGTGGCGGT GCATGACGTA GCTAGTCACA GGATGGCAGT TGAATTTGCC	2220
TCTGCCATTC GTCTGGCTGA TGAAGCGGAA AATTTAGATT TAAACAATA TAAATTAAGT	2280
GAAAGAAATT GAAACAATC AGTGGATTGC TAATACCGG ACGGATCAAC CGCATTTTGG	2340
CTTGAACGA ATGGTGGAAC TGTTAGCTTT GGTGGCAAT CCCCATCTCA AACTCAAGGT	2400
CCTCCATATC GGAGGGACTA ACGGCAAGGG CTCGACTATT GCTTTTTTGA AAAAGATGCT	2460
AGAAAGCTA GGGTTGAGAG TTGGCGTGT TAGCTCGCCC TATCTCATTC ATTACACAGA	2520
CCGATTATG ATCAATGGGG AATCGATCTC AGAAGCGAGG CTAGAGCTC TCATGGCAGA	2580
CTATCAGTCT TTGCTGGAGG GAGAAAGCGT CGCCAATTTA CAGGGCACAA CCGAGTTTGA	2640
GATTATCACA GCCCTGGCTC ATGACTACTT TGCTCAGAG CAAGTAGATG TGGCCATCAT	2700
GGAAGTTGGC ATGGGTGGAC TTTTGGATAG TACCAATGTC TGTGAGCCCA TTTTGAACGG	2760
AATTACAACT ATTGGCTTGG ATCATGTGGC TCTACTTGGT GACACCTTGG AGGTATATGC	2820
AGAGCAGAAG GCAGGTATTA TCAACAAGG GATGCCCTGT GTAACAGGGC GTATTGCTCC	2880
AGAAGCCTTG GCTGTGATTG ACCGCATTCG GGAAGGGAJA GATGCGCCGA GACTTGCCCTA	2940
CGGACACAGT TATCAGGTTT GTCAACAAGA AAGTGTGGTG ACAGGGGAAG TCTTTGACTA	3000
TACAAGTGCT GTGACACAAG GTCGCTTCCA GACTAGCCCTG CTTGGTTTGT ACCAAATAGA	3060
GAATGCTGGG ATGGCCATAG CTTTACTTGA TACTTTTTGT CAAGAAGATG GTGAGAGCT	3120
AGCAAGCAAT GATTTCTTGT GTCAAGCCTT GGAAGAAACA AGTTGGCCAG GCGGTTTGGGA	3180
AATCGTGTCA AGAGATCCCT TGATGATTTT GGATGGAGCC CACAATCCCC ATGCTATCAA	3240
GGCCTTGTTG GTAACCTTGC AAGAAGCTTT TGCGGATTAT CATAAAGAAA TCCTCTTCAC	3300
TTGTATCAAA ACCAAGGCCT TGGAGGATAT GTTGGACTTG CTGGGAGCCA TGCCAGTTAC	3360
CGAGCTTACT CTAACACATT TTGCGGATAG TGGGGGACG GATGAAACG TGCTGAAGAG	3420
GGCAGCTAAG TCTAGAAATC TCAGCTACCA AGATGGCAT GATTTTCTAG AGCAAAATTT	3480
GACAGATAAA AAGAAGAGA AACAAACAGT TAGGATTGTC ACAGGTTTCT TGTATTTCTT	3540
GAGCCPAGTG AGGCCTATC TGATGGAGAG GAAGAACGAG AATGGATACA CAAAAGATTG	3600
AAGCGCTGT AAAAATGATT ATCAGGCTGT TAGGAGAGGA CGCTAATCCG GAGGCTTCC	3660

AGGAAACACC	TGCTCGTGTA	GCCCCTATGT	ATCAAGAGAT	TTTTTCAGGT	CTTGGTCAAA	3720
CAGCAGAGGA	ACATTGTGCA	AAATCCTTTG	AAATTTATGA	CGATAATATG	GTGGTAGAAA	3780
AGGATATCTT	TTTCCATACC	ATGTGTGAAC	ACCACCTCTT	GCCATTTTAT	GGTAGAGCGC	3840
ACATTGCGCTA	CATTUCAGAT	GGTCGTGTGG	CAGGCTTGTC	TAAGCTAGCC	CGTACGGTTG	3900
AAGTTTATTC	AAAAAAACCA	CAAATTCAG	AACGTTTGAA	TAATCGAAGTG	GCGATGCGCT	3960
TGATGGACTA	TCTAGGTGCT	AAAGGAGCCT	TTGTGTGCAT	TGAGGCGGAA	CATATGTGTA	4020
TGAGTATGCG	TGGTGTTAGA	AAACCAGGCA	CTGCAACCTT	GACGACAGTA	GCTCGTGGTC	4080
TATTTGAAAC	AGATAAGGAT	CTCCGTGACC	AAGCTTATCG	TTTAATGGGG	CTATAAAAAG	4140
AATCCGCTTC	AAGCGGATTT	TTCTAGAAAG	GAATCATTAT	GGATCAACTG	CAGATTAAGG	4200
ATTTGGAAAT	GTTTGCCTAT	CATGOTCTTT	TTCTAGTGA	GAAAGAAATT	GCGCAGAAAT	4260
TTGTGCTTTC	AGCCATCCTA	TCCATGATA	TGACCAAGGC	AGCTACAGAC	TTGGATTTAA	4320
CAGCCTCTGT	CCATTACGGA	GAATTGTGTC	AGCAGTGGAC	GACTTGGTTT	CAGGAACGGA	4380
GTGAAGATTT	GATTGAAACG	GTAGCCTATA	AACTGGTGGA	ACGTACCTTT	GAGTTTTATC	4440
CTCTTGTCCTA	AGAAATGAAG	TTGGAACCTGA	AAAAACCTTG	GGCACCGGTG	CATTTGTGAC	4500
TAGATACTTG	CTCGTAAACC	ATTTCATCGCC	GCAAGCAACG	AGCCTTTATC	GCCCTAGGAA	4560
GCAATATGGG	AGATAAACAA	GCAAACTTGA	AGCAAGCCAT	TGACAAATG	CGAGCTCGTG	4620
GCAATCCATAT	TCTCAAAGAG	TCCAGTGTCT	TAGCGACGGA	GCCTTGGGGT	GGAGTGGAGC	4680
AGGATAGCTT	TGCCAATCAA	GTGGTTGAGG	TGGAACCTG	GCTACCAGCA	CAAGACTTGT	4740
TAGAAACCTT	GTTAGCCATT	GAGTCAGAGC	TGGGACGGGT	GAGAGAAGTG	CATTGGGGAC	4800
CTCGTTTGAT	TGATTGGGAC	TTGCTCTTTG	TGGAGACCA	GATCCTTTAT	ACAGACGACC	4860
TCATATPTGCC	TCATCCTTAC	ATAGCGGAAC	GCCTTTTGTG	CCTTGAGTCT	TACAGGAAAT	4920
TGCGCTTCAT	TTTATCCATC	CGATATTAAA	ACAACCGATC	CGCAACTTGT	ATGATGCTTT	4980
GAAAAAATAG	AAAAACTCTA	GTTTTCAGTT	ACTTGCACAT	GAAGGCTAGA	GTTTTATATC	5040
TCTTCGAAAA	TCTCTTCAAA	CCACGTGAGC	GTCGCCTTAC	CGTACTCAAG	TACAGCTTGC	5100
GGCTAGCTTC	CTAGTTTGCT	CTTTGATTTT	CATTGAGTAT	TAAAAATAGT	CATTTTCTTC	5160
TGGGAGGAGG	ATAGTTTCTC	TACCGTCCAT	GTCTAAAGCC	AGTACTCTTG	GGGGATAACG	5220
AGGGTCGAAA	GGATGGTTAA	AGTCAAAATC	AATGGCTGTA	GGGAGGTGTT	GACTTTGAAA	5280
TGGGAAGGTA	ATCTPTCTCT	GGTTATTTAAG	CANPTGAAC	TCGAGTCTTT	CTTCCAATTTC	5340
AAAGACATTT	TTTAAAGAAAT	GGTCGATGAT	ATACCAAAAA	GAGTCAATGA	TGTCATCAGG	5400

1298

CAAGCTGGTA ACAATACCAA AACTAGCAGA TCGCATGTGG GTATTGGTAA AAGCCAATAC	5460
TCGTGCCCT TCTTTTCCC TTATCATACA GCAATAGGA TTAAAAATCA AGAAAGGTG	5520
ATTTTTTGA AAGGATTTTA GTTACAGGGA GAAATAGGGA AAAAATTCCT AAAATCTAC	5580
CGAAGTTAAT AGGTAAATTC CCAATTAAC TTGATTATAT AACTTTCAGT TACITTTGAGA	5640
AGTTACCGAA AATATTTTTT CATATCTATT GACTTTTAGG GGTAAATTT CGTATGATAG	5700
TAGGCGGTAT TGTTTACCC ATTTGAAAG CCCCGAACC TTCCAAATAC TTTTCGATGG	5760
GAAGGAACAC CCATCAGCT AAACAAAAT CGAATATAT ATAGGAGAA TCATGAACAA	5820
AACAACATT ATGGCTAAAC CAGGCCAAGT TGAACOTAAA TGGTACGTAG TTGACGCAAC	5880
TGATGTACCA CTTGGACGTC TTCTGCAGT AGTTGTAGC GT	5922

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1988 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TAACATACCTA CGATGAGCTG TTGTGATTCT CATTAGTCC CCTTCCCAA GAGGCATAGG	60
GGTGCACATA ATAGATGTGC TCCTCAGAAA ATATATCAAA CAAGCGATTG AATTCGTTTC	120
CATTATCTGC COTGATCGAA AGAATCTTGT GTTGTTTTAA GATGAGTTT AGAGCCTGAT	180
TGACCACCTC AGCACTTTTA TTGGAATCA ATCGGATGAT CTGATGCTTA CTCCTTCGAT	240
CCGTCAAGAC AATCAAGCAG TAGTTTTTCG ATCTCGTAAG TAGAACCTTA TCAATCTCAT	300
AATGCCCATT CTCCAAGCGA AGATTGATAG CTTCAGGCCG CTGTTGAGTG GATTGACCAG	360
CAGGTTTAAA GTTGGTGCTA GCCTGTTTCT TAAGCGCTTT TCCTTTCTTA GGGTAAAGCA	420
AATCTGCTT GCTTAACCCC AATTTTCCAT GATGAATCCA ATAGTAAATG GTTGAAATTC	480
CCACGTTAAC CCCTTTAGCC ATAACCATCA TTTCAGCGGA AAATTTTGG TTATGATAGT	540
GGAGAATCTT TTCCTTTAGT TCCTTGGTCA AGCTTGATTT CTTGACCGAG GCCTTCCGAT	600
TGTTTTTATA AGACTGTTGA GCGTAGTCGG CAGAAATAAC CTCCTTTGAAG CGCCCTTTTC	660
CAAGACATTG TCGGACTGTC CCACGCTTGA TTTCAGTGTG ATAGTTTGAG GAGCTTTTTC	720
AAGTAGAGAG GCAATTTCTC TATTTGATTT TCCTTCTTTT TTCCATCTTT CGATTAAGCG	780
ACGGCTATCG ATTGTCAAT GTTTGGCTTT TGTAGTATAA TTGTCTTGCA TCTCTGTGCC	840
TTTCTGTGT TTGTGGTTGA ACAACAAGTA TAACACAGAG GTGCTTTCTT ATGCCTACAA	900

1299

GAGCTTCAT TATTTCATT TTCTTTTGGG TTTCACCTCA TTCTGAAAAA CTGTGTGATA 960
 TTTACTGAAG CTAGCAAGTC TTACCTGTAA ATTTAATGAA AGCAACACAA AATCCGAGAG 1020
 GGGAACTCG GATTAATAGA TAGAGAGTTT TTAGTTTAAA TAAATTGTTT AAAATATCAA 1080
 CAACATCACT TCTTTCTTA ACCTGATAAG TCTTGATTCC TAATTTTGGG GCTACGATTA 1140
 TATGTCTCTC AATATCGTCT AGAAAGACAC AATTCTAGG TTATACCTGG TATTTATCGA 1200
 TAGTTACTCA TATACATCAG TCCACCTCCA TACTTATGTG CGAGCCTCTC TTTGTATTAT 1260
 ACCTCCATAC TCACCTTACA GATTCTTTTG GTAAATATAT CTTTGCCTAA TGTAGAGACA 1320
 GTCTTGCAAA GAAAAAAGT CCTGTAGCC ATGTTTCTGA TAAAGTCCG GTGCTGGA 1380
 CTGGTAAGTA TTGACAAAGG CAACAAACA ATTCGATTC TTAGCTTAC TTTCTGCCTG 1440
 TTGCAATAGT TTTGAACCGA TTCCTTGCCC TCGAGTTCC TCTTTTACAA ACAAACTACT 1500
 GATTCTTAGC CAATTCCAA AAGTCTCTGC TATCAAACT GCCAGGAGT TCCCTTTTTC 1560
 ATCTTCGACA TAAAGATTAA GTGGCTCACT TTCAGCTCT TCTCTTTTTC AACGGTTATA 1620
 AACACGAATC AGATTCCCTA TTTCTTGCGA TTTATGTGAT TCCTTATTTT CCAATCTAAA 1680
 GTATAGTGAA ATGAAATAAA ACATGCGCAA ATCGATTAG GAATTTAATC TAATTTCTAA 1740
 CAATGTCTTA GAAATCAAAG TGTACTATTT TAACTTCAAT GCATATACA TCTAATACTA 1800
 AATAAAATC AAAGAGCAAA CTAGGAAGT AGCCGAGGT TGCTCAAAAC ACTGTTTTGA 1860
 GGTGTAGAT AGAACTGACG AAGTCAGCTC AAAACATAGT TTTGAGTTG TAGATGAAC 1920
 TGACGAAGTC GGCTCAAAAC ATGGTTTTGA GGTGTAGAT GAACTGACG AAGTCAGCTC 1980
 AAAACAGG 1988

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CCGGATATT GTTTATGTA ATTTCTTGC AAGTTTCTT TTAGTAGCTT GTCAGTCAGG 60
 TTCTAATGTT TCTCAGCTG CTGTGATGC TATCAAAAC AAAGGGAAAT TAGTTGTGTC 120
 AACCAGTCTT GACTATGCAC CCTTTGAATT TCAATCATTT GTTGATGGAA AGAACCAGGT 180
 AGTCGGTGCA GACATCGACA TGGCTCAGGC TATCGCTGAT GAACCTGGGC TTAAGTTGGA 240

1300

AATCTCAGC ATGAGTTTGT ACAATGTTT GACCACTCTT CAAACTGGTA AGGCTGACCT	300
AGCAGTTGCA GGAATTAGTG CTACTGACGA GAGAAAAGAA GTCTTTGATT TTTCAATCCC	360
ATACTATGAA AACAAGATTA GTTCTTGCT TCGTAAGGCT GATGTGGAAA AATACAAGGA	420
TTTAACTAGC CTAGAAAGTG CTAATATTGC AGCCCAAAA GGGACTGTTT CAGAATCAAT	480
GGTCAAGGAA CAATTGCGAA AAGTTCATTT AACTTCCCTA ACTAATATGG GTGAAGCAGT	540
CAATGAATTG CAGGCTGGAA AAATAGATGC TGTTCATATG GATGAGCCTG TTGCACTTAG	600
TTATGCTGCT AAAAACGCTG GCTTAGCTGT CGCAACTGTC AGCTTGAAGA TGAAGGACGG	660
CGACGCCAAT GCCGTGCTC TTAGAAATA GTGATGATTT GAAAGAAGT	709

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1680 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

TATAAAATGT TAAGTTAAAT GATTTCAAA TTCAGAAAGG GATTGCTTTA TGCAGTTCCT	60
TTTTATTTTA ACAGGAGTGA AACTATAGTG TTTCTAAATT GTGAATCAAT CAAAACGTAT	120
TGTGATGGGG CTATCTTAGC TTAGAAAC TTCAAAATTT AAAATTTAAG GCAATCAATT	180
ACTTGAAGA GTATGAAAGC ATTTAGTTTA TAGGAATTC AGGTCTAGAA TTACATATAG	240
ATATTTATGA AGACGGGCTG TTCGATAGTT AGTATTGTTT TATTCTGAAA GATTTGAGCT	300
GTCAAGTTGA TAGAAAGTGT TCGAATTTTT TTAAGTGATT AAATTAGTTA ATTGTATGAG	360
GTGCTTTATG ATATAATGTT CTTAATGAAT TTTCAGAAAG GAAAACCTCA AATTGTTCTA	420
CAAAATTTCTA CTCCTTGACC TCGACCACAC TCTTCTTGAT TTTGATGCTG CTGAGGATGT	480
GGCTTTGACC CAACTTCTAA AAGAAGAAGC AGTTGCGGAT ATTCAGGCTT ATAAAGATTGA	540
TTACGTTCTT ATGAACAAGG CTCCTTGAA AGACTTGAG CTGAAGAAA TCAGTAAACA	600
AGAGCTGGTT AACACGCGCT TTTCTCGTTT ATTTGCTCAT TTTGGACAGG AAAAAGACGG	660
TAGTTTTCTT GCCCAGCOTT ACCAATTTTA CTCGCCCCAG CAGGACAAA CACTATCGGG	720
CGCTCATGAT CTCCTTGACA GCCTCATTGA GCCTGATTAT AACTTGTATG CTGCGACAAA	780
TGGCATTACT GCCATTGAGA CAGGACGTTT GGCTCAATCT GGTCTAGCAC CTTATTTCAA	840
TCAAGTCCTT ATCTCAGAAC AGTTGCAAC TCAAAAGCCG GATGCTCTTT TTTATGAAAA	900
GATTGGCCAG CAATTTGCTG GATTAGTAA AGAAAAGACG CTGATGATTG GAGATTCTCT	960

1301

AACCGCCGAC	ATTCAAGGTG	GCAATAATGC	GGGATTGAC	ACTATCTGGT	ATAATCTCTCA	1020
TCACCTCGAA	AATCACACAC	AAGCCGAGCC	GACTTACGAA	GTCTATTCTT	ACCAAGACTT	1080
GCTGGATTGT	TTAGATAAAA	ATATTCTTGA	AAAGATCACA	TTTATAAGGA	GACGAGCTAA	1140
TGACTACAAA	AAAGCTAATA	TTACTATTCA	ACAGTACATT	GAAATGTCTG	ANGTTGATTT	1200
TAATGAAGCT	GTTAATTATG	AATTTACATC	TGCACTTGTG	CAATTAGCAA	ATAGTATTTA	1260
TCAATCTCTT	TTTAAGTTTT	TTGATAAGAA	AAATTTCTCT	GGCGATTTAA	TTTTTACTTG	1320
GAAATCTCCA	TCATTAGTCA	AAGAAGGGGA	TTATATTGGG	AGAAGGGATT	CACAAGTAGA	1380
TAATCTTAGA	GTAATAGGAA	ATATAATTCC	GAATATCTTT	ACTAATCGAA	AATATAGCCT	1440
CAATATGAAT	CGTAATGGCT	GTATGGGAGA	TTTTCTCAT	GACTTTTTTG	ATATATACCT	1500
AGATCATGTA	GCAAAATATG	CCTACGACAA	AAAAGTTAAT	AATATTAAAG	AGTATTATCC	1560
TTTAAAAAGA	GCGATTTTAC	ACCAAGAGAA	TGCATTGTAT	TTTCGATTTT	TTTCTAATTT	1620
TGACGACTTT	TTAGAAAAAA	ATTATTATAA	GACTATATGG	CAAGTTTCTA	AAAGAACTCC	1680

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

AGCTCGGTAC	GTAGTATnTG	TGGTGCAATA	ATGAGTGAAA	AGAGGATAGA	GAGGATGAGG	60
CCGATAAGAA	CACCGGTAGC	TGCATCGTGA	AATACTTGTT	TTTTCATAGT	TCTAATTTCT	120
CCTTGATGCT	TTTTAGATAA	CGGCGTGAAG	AGTAGGTGAA	GCTTTGTTTT	TTCAAGAAAA	180
TTTTCTACCAG	ACCGTTGGC	GTGagCTTGA	GSTGAGAGAT	GGAATCGATA	TTGATGATTT	240
CTGATTGGGA	AATTGTGATA	AAATTGGTTG	GCAAGAGTTT	AAGAACTGGA	TAGAGTCGCA	300
AATCAATGCT	GTAGGTCTGA	CTCGCGGTTT	CTGCTAGAAC	CTTCGATTC	TCGATATAGA	360
AGCGCTGAAT	CTTGCCAATC	TCACTAGAT	AGACCTGATC	ATCGATTTTT	CCTTGATTTT	420
TTTTCTCTTG	GTCCAGATTT	TCTGCGAACT	CGATGACTTT	CTGGACTTTT	TCGGTTCTTT	480
GAGGTGCTTG	GACAATCAGC	TTTTCCCTCT	CGTAAGTCTC	ACTAATCTGT	AGTTCTACTT	540
TCATAGTTTT	CTCTCCTTTT	CAGTTATACA	AGGTTGTGAT	CACCTTCTGT	ATATCCGG	598

(2) INFORMATION FOR SEQ ID NO: 272:

1302

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CCAGCAATC AATAACTGCA ATTGCTATAA AATGGATTCT ATAGAGTTTT TTCATGACAA	60
GACCTCCCTC TTTTATCTAA CTTCATTCTA CTCCAAAAGA ATGGGAGTTA CAACTAAAAAT	120
GATAAAAATA GCAGAGGGA GATTCTCTTA AGTTGGCTAG TATTCTTTAT TTGAGTTTCC	180
TTCTATTATC TAACTTCTTC ATCATTCCAG ACAATAAAG CTCCGATTGC ATTGAGGATA	240
TAAAAGATGT ATTTACCGAT ATTGGCGAAG TTTCCCTTGA TACCAGCTTT TGTGAGCTGA	300
ACGAAATGT AAATCAACCA AAAGCCCCAC TGAGTTGTTA GTTTTAATGC ATTCAAAGCA	360
TTGGCAATGA GGCACAGTGC AAAGGCAATA GTTGTACGT AGGCAAGGA ATTCATCTTG	420
CCCCCATATC CGATATAGTT GGTCACAAAG GCAAAGAGGA AGGCGATGAT GGAATGATG	480
ATGGCCGCCA ATTTTACCTG TTTTGGCTC ATTTGGTTGG GTCTGCCTTC TTGCGAAGCT	540
TCCCACTTCT TTATAGCAAA GGTATAAATG AGGAAGGTGA CGGGATAGGT AATGATGGCC	600
GCCTTATTTC CAAGGATATA ATCAATAGCA CCGGACAAAA TGGTATTAA CATTACCAAG	660
TAAATTCCCC ATTTGCTTAA TTTCCCGGTG AAACGAGTGG ACAACATGGA AATCCCAAG	720
TTGGTTACGG AAATCAATCC AAAGGGTACA AGAGCTGTCC ATGATCCCCA GTCTACAAAT	780
TTATCGAGGT GTGAGTTGAG GTAACCATG GCAATCGCAA TCCCAACGAC CAAAGCAACC	840
CCGAAGAGGT CAAACTATTT AGATGTAGCA AAAATTTTGA GTGATTTTTT CATAGGTTAA	900
ACTACCTTTC TTTTTTCAA ATATTCTCCC ACCAAATGAA AGTAAAAATA AATGATAGAA	960
ATAAAACCCCT GAAAAATAAG GTTCTATAAT ATTGTAGTGG GGTAAATCCA CTATAGATAT	1020
TATGGAGCCT ATTTTATTGT AGAAAAAAG TCCCATATGA CCTATAATGA AAAGCGACAA	1080
AACAACATCAT TAGAAAGAT	1099

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CTGGGATTCA CGTGGAAAGG AAGCCCAGAG AGTAGCCAGG TGFACTGCTA GAACAGTGAG	60
TGAAATTGAA TATTACCATA GAGAGTCAAC CCAGATAGCT CAGGCTTTAG TTGAAAAATCA	120
AGCTCGTATC GAGGGAATCT ATAAATACTT TAGCCTTAGC ATGCCAGACT ATTTTACTTG	180
GCAATTAGAG CGGAAAGCTT CGCCTTATAT ATCAGTCTCT CTGTATGAAA ATGTTGATGA	240
CCTCTATGTT CGAAATGATT TTGTAACTGG GGTGGCCATT GCTTTTCAAG ATTACAAGGA	300
AGTCTATGTT TCTACTAAAG ACRAACGTAG GkAGAAAAA ATCAGGCGTG AGGAATTTCAA	360
ACCAGCAGGA AATAGTTTTG CCATTCAGT GTCAGATCCA GTGTCAGATC AAGACTTAGG	420
AGTGATTTAC ATCTCCTTGG ATCCTGCTGT TTTATACCAT GCCATTGATA ATACTAGAGG	480
TCATATCCG ATGGCAGTAA CAGTGACCTC ACCTTTTGAT ACGGAGATTT TTCATATGGG	540
TGAGACAGTT GATAAGGAGA GTGAAAATTG GCTAGTTGGC TTAACCTCTC ATGGATATCA	600
GGTTCAGGTG GCAGTCCCTA AAAACTTTGT TTTACAAGGA ACAGTGACTA GCTCTGCTTT	660
GATTTGTTGGT TTGAGCCTTC TCTTTATTGT CMTCTTTAT CTGACTTTGA GGCAGACTTT	720
TGCTAATTAC CAAAAGCAGG TAGTGGATTT AGTAGAATCC ATTCAAGTCA TTGCTCAAGG	780
CGAAGAGGGG CGTCGGATTG ACATTTCCGA GAAAGATCAG GAATTACTCC TAATCGCGGA	840
GACGACCAAT GATATGTTGG ATCGATTGGA AAAGAATATC CATGATATTT ACCAGTTAGA	900
GCTTAGTCAA AAAGATGCCA ATATGCGAGC CTTGCAGGCG CAAATCAATC CTCATTTTAT	960
GTATTAATAC CTGGAGTTCT TGGCGATGTA TGCAAGTTATG CAGAGTCAAG ATGAGTTGGC	1020
AGATATCAAT TATGAATTCA GTAGTCTCTT GCGTAACAAAT ATTTCCGACG AAAGAGAGAC	1080
CCTCCTCAAA CAGGAATTAG AATTTTGCCG TAAATACAGC TATCTCTGCA TGGTTCGCTA	1140
TCCCAAGTCC ATTGCCATAT GTTCAAGAT AGATCCAGAG TTAGAGAATA TGAAGATTCC	1200
CAAGTTTACC TTGCAACCGC TGGTAGAAAA CTATTTCCGC CATGGTGTG ACCACAGGCG	1260
GACAGATAAT GTGATTAGCA TCAAGGCTCT TAAACAGGAT GGTTTGTGG AAAATTTGGT	1320
GGTCGATAAT GGTAGAGGAA TGTGCGCTGA AAAGTTGCA AATATCCGAG AAAAATTAAG	1380
TCAGAGATAT TTTGAACACC AAGCCAGCTA CAGTGATCAA AGGCAGTCTA TCGGGATTGT	1440
CAATGTACAC GAGCGTTTGG TGCTCTATTT TGGAGACCG TATGCCATTA CTATAGAGTC	1500
TGCAGAGCAA GCCGTTTTC AGTATCGTAT TACAAATCAA GATGAGTGA AAGGGAGAAA	1560
ATGTATAAAG TATTTATAGT AGATGATGAG TACATGGTGA CAGAAAGTCT GAAGCGTTTG	1620
ATTCCTCTTG ATAAATGGGA TATGGAGGTC GTCCCAACAG CCAATCATGC CGATGAAGCT	1680
CTAGAATATG TTCAGGAAAA TCCTGTCGAT GTCAATCATTT CCGATGTCAA TATGCCAGAC	1740

1304

AAACACGGCC TTGATATGAT TCGGAGATG AAAGAGATCT TACCAGATGC TGCCATATATC	1800
CTGCTCTCAG GTTATCAGGA GTTTGATTAT GTAAAAAGAG CAATGAACCT TAGTGTGGTG	1860
GACTATTGG TCAAGCCGTG TGATAAGTA GAGCTGGAA ATCTGCTGGA GAAGATTGCA	1920
GGTCAGCTCG GCGAGAGAGG GAAGAAAAGT CAGACTCTTA GTCAAGAAAT AGACGAGGCT	1980
GGATTTGTGA GTTATTTAGG GGATAAGGAG AATTGGTGGA TAGGTCTATC CAAGGAAAAA	2040
CAAGGTTCTC TCACCATTCC CTACTATGTC TTGGGTCAAG ACTGGCAGAT TTTCATTTCT	2100
GGCCACCCCC TAGATGGTTT AGTCGTTACA CCTTTTGAAG CTCCTTATCA AGAACACTTT	2160
GAACGCTGGA AGCTGAATGC TGAGAAAACC CTCCTTTACG GTTCTGTAAA TCTGCAGCAG	2220
TCTGAGAGTC TCTTTGCCTA TTACGAACCG ATTTATAGGG TTATCATTCA GGGAAATCTC	2280
AATCAAAATG TAGAAGAGTT AAATCTCTTG GAGAAAGTAG TTCTTGAAAA TACACCTCGT	2340
GTTCCTGATTA CTAAACAGCT TTTTATCCAG TTGTGTCATG ATGTTTCCCA TTTATTTGAA	2400
CATCTCAAAG CTGATGATAT GACGGACATT GTCAAAACCA TTCAATGCTAT TCAATCCCTC	2460
GATGAATTGG TTTCTTATAT CAAGGAAACT CTGATCAGCT TTTTCGGTCA ATACCGTATG	2520
AATGAAAATG TGGTCAGTGT GCTGGAAGTC ATTGGTCGTG ATTACCAAAA AGAGCTTTCC	2580
CTCAAGGATA TCAGTAAGGC CCTCTTTATC AATCCTGTCT ATCTAGGGCA GTTGATTAA	2640
CGTGAAACCG ATTCCGACCT TGCAGAGTTA CTAACAACAC AACGTATTAA GGCTGCCACG	2700
CAGCTCTTGC TTTCAACTAG TGA	2723

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 836 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CCGACGTTTT TTTAAACCGT ATATAAGTAT AGCATAGTCA AAAAAAGAAT GCAAGATTTT	60
TGCAAACTTT TTTAAATTT TTGTAATTT TTCTTTTAAA GTTCTACTGT CAGGACTTGA	120
CCTTGCTTAA CAACCTGTTT TCCGGCGATA TAAACATCAT CTACATCACT AGATTAACT	180
GCATAAACCA GGTGAGACAG CATATTTTCC TGAGGTGGA GATGAATTTT CCCTTGTGGT	240
TGAATGACCA GAAAACTGC TTGCTTGCCG ACTTCCAGAC TTCCTATCTG ATTTTCCATT	300
CCAAGGACCT TAGCCCCCTC GATTGTCACT ACCTTGAGAG CTGTTTCGAT TGGAACTGG	360
CTGGCATCCC CACTTTTCAAT CTCTGAAGA AGAGCTGACG TCCTTGCTTC CTCAAACATA	420

1305

TCTAGATTGT TAFTTGAAGC AACCGAGTCA GTCCGAATTC CGACTGCTAC TCCCGCTTTT	480
TGGAGCTGGA TAATTTGAGC AATTCTGTAT GCCAGTTTGA GGTACTGAT AGGATTGTGG	540
GGATAGChA CTTGAGAAGA TGCCAAGCGT TCAATTCTCT TCTCGTTTAA TTGACCCCG	600
TGAGCAATA CGGACGGATG ATCTAAATAA CCCAGTCTTT CAAGAAAGC AAGGGGGCCT	660
TTGCCGTATC GTTTGAGGAT AATTCTGTAC TCCTCCTTGG TCTCCGCCAC ATGACACATG	720
AGCGGAATAT TTAGCTCTTT TGCCATTTC AAATCGTCT CCAGCAAGTC TCTACTGCAG	780
CTATACGGAG AATGAGTGCC TACCATAACC TTGAAATTTG GATTTTTATA TTTTAA	836

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

ATTTTTATTTC ACTTTT TAGG TGCTCTGGG CTATCTTAT ATAGChTCAA GACCATGGGA	60
GACGGTTTAC AACAAAGCTGC TGGAGATCGC CTGGGTTTTT ACATGACAA ATATACTAGT	120
AATCCCTTGT TTGGAATTCT GGTGTGTAAT GGGATGACTG CTCTAATTC A GTCTAGTTCT	180
GGTGTAAACAG TTATCACAGT CGGCCTGGTC AGTCCGGTTC TCTTAACCTT ACCTCAGGCT	240
ATCGGGATTG TCATGGGTGC TAATATTGGG ACAACTGTCA CATCCTTTCT CATCGGTTTT	300
AAATTAGGTA ACTATGCCCT ACCTATGCTC TTATTCGGTG CCGTCTGTCT TTTTTTTACG	360
AAAAATCGGA CAGTCAATAA TATCGGACGC ATCCTCTTGG GTGTCGGTGG TATCTTTTTT	420
GCCCTCAATC TCATGAGCGG CGCAATGGCT CCACTCAAGG ATTTACACAT CTTTAAAGAC	480
TATATGATTG AGCTAAGTAA GAATCCTGTT TTGGGTGTCT TTGTCCGTAC TGGCTTGACC	540
TTGTAAATTC AAGCTTCTTC GGCTACCATT GGGATTTCAC AAAACCTCTA CGCCGGCAAT	600
CTAATGTATC TACAGGGAGC TTGCGCAGTT CTATTTGGTG ACAATATCGG GACAACCAT	660
ACAGCCATCA TTGCCTCTTT AGGGGCTAAT ATTGCAGCTA AACGGGTAGC AGGAGCTCAT	720
GTTCCTTCCA ACGTATCGG AACAGTTGTC TGCTTATTTT TTCTAGTTCC TTTTACTGTC	780
CTGATTTCATT GGTTTGAAGC TAAGCTAAAT CTAGACCCGG AAATGACCAT CGCCTTTGCT	840
CACGGAACCT TTAATATTAC CAACACCATT GTCCAATTTT CATTTATCGG AGCTCTGGCT	900
TACTTTGTAA CCAAGATTAT TCCTGGAGAG GACGAGGTTG TCAAAATACA ACCCTTATAT	960

1306

CTTGATGAAC ATTTCAATCAA ACAGGCCCA TCTATCGCTC TAGGAAATGC TAAGAAAGAG	1020
CTCTTGGACT TAGGAAACTA CGCTGCTAAA GCCTTTGACC TTTCCTATAA GTACATCATT	1080
GACTTGGATG AAAAAGTTGC TGA AAAAGGG CATAAAACCG AAGAAGCAAT TAACACCATC	1140
GATGAGCAAT TAACACGTTA TCTCATTGCC CTTTCAAGCG AAGCTCTCAG CCAAAAAGAA	1200
AGTGAAGTGC TTACCAATAT CCTTGATTCC TCCCTGATT TGGAAACGAT TGGAGACAC	1260
ACGGAGGCTC TACTCAATCT GACTGACTAT CTTCAACGGA AAAATGTGA ATTTTCTGAT	1320
GCCTGCTTGA AAGAATPAGA GGAAGTTTAC CGCCAACTA GTGACTTTAT CAAAGATGCT	1380
CTGATATAGT TGGAAAACAA TGATATTGAA AAAGCACGCA GTCTTGTAGA ACGTCATGAA	1440
GCAATCAATA AGATAGAACG TGTTCCTAGA AAAACCCACA TCAAAACGCT CAACAAAGGC	1500
GAATGTTCAA CACAAGCTGG GGTCAACTTT ATCGACATCA TCTCACACTA CACTCGTATA	1560
TCAGACACAG CTATGAACCT TGCTGAAAAG GTTTTTGCGA ACAAAATCTA AGAACCAGAA	1620
AGCTATCCAT CATATTTGGA TGGCTTTTFA CTTTTTCTTA AGCAAGACTA GATGAATACA	1680
AAC TGAAAGA GTATTCTGCA GATATATAGT CCCCATTAT TCACCCCAA TCTAAAAACC	1740
ATCCAGAAAT CTTGCCCTTAG CTTAGATCCT GGATGGTTTC TTTTTTCAAC CAATGGGTGT	1800
TTTTTACTAG AAAAAAACA GTTTCCCTTT TATGATATAA GTGTAGAAAA AAACACAAAA	1860
AGAAAGGAAA CTCACATGAA CAGTTTACCA AATCATCACT TCCAAAACAA GTCTTTTTAC	1920
CAACTATCTT TCGATGGAGG TCATTTAACC CAGTATGGTG GTCTTATCTT TTTTCAGGAA	1980
CTTTTTTCCC AGTTGAAACT AAAAGAGCGG ATTTCTAAGT ATTTAGTAAC GAATGACCAA	2040
CGCGCTACT GTCTTTATTC GGATTGAGAT ATCTTTGTCC AGTTCTCTTT TCAACTGTTA	2100
ACAGGTTATG GAACGACTA TGCTTGTAAA GAATTGTCAG CTGATGCCTA CTTTCCAAAA	2160
TTGTTGGAAG GAGGGACGCT TGCTTCACAG CCAACCTTAT CCCGTTTTCT TTCCAGAACT	2220
GACGAGGAAA CAGTCCATAG TTGCGATCC CTCACCTTG AATgKCGAA TTCTTTTTTAc	2280
AGTTTCACCA GCTAAACCAA CTCATTGTAG ATATCGATTG TACCCATTTC ACAAC	2335

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CGGATTCACT GTTCTTGACT AATCAATAAC ACAGTAGAAA ATCTCACAGC AGTCATTATG

60

1307

TTGCTTTTCA TACTAGGCAA GTGACTGAGG CTTGTACTTG CGTACAGCAA GGGAGCTTAA	120
GGCCGTAGAA GAGAAAAATA GTAGACTGAA AAGCCGCAAG ACTTCATCAT TTCGAGAAGT	180
GACGTGGAG ATGAAAAATCG ATTGAACCACT TTACAAGGAG AATAGAAAAA GGCTAAAAAA	240
AGCAAAACAC TTCGTGCTGC TCTTGAGAAA ATGACAGCA CAAAGCATA CAGTGTAGAA	300
GAAGCTGTAG CACTTGCAAA AGAAACTAAC TTTCGAAAAA TTGATGCAAC TGTAGAAGTT	360
GCTTACAATC TGAACATCGA CGTTAAAAAA GCTGACCAAC AAATCCCTGG AGCAATGGTA	420
TTGCCAAAGG GTACTGGTAA AACTTCACGT GTTCTTGTTT TCGCACGTGG TGCAAAAGCT	480
GAAGAAGCAA AAGCTGCTGG TGCAGACTTT GTTGGTGAAG ATGACCTTGT TGTAAAAATC	540
AACGACGCTT GGTTCGACTT CGACGTAGT ATCGCTACAC CTGATATGAT GGCTCTTGT	600
GGACGTCTTG GACGTGCTCT TGGACCACTG AACTTGATGC CAAACCCATA AACTGGTACT	660
GTACAATATG ATGTTGGCAA AGCGGTGAA GAGCTAAAG GTGGTAAAAA CACTTACCGT	720
GCTGACCGTG CAGGTAACGT TCAAGCAATC AT	752

(2) INFORMATION FOR SEQ ID NO: 277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GTCAACATTG ATTTCAAGGC TGTTCGCTTT CTATCTCCCC TTTTTCATAA TGTATAATAA	60
AATGAAATAA TAACAGGAGC AATTGATCGG GACAGTCAA TCGATTTCTA ACAATGTTTT	120
AGAAGTAGAG GTGTACTATT CTAGTTTCAA TCTACTATAT TTTCGTACAG GTGCTTCAAC	180
CATTGTGAAG ATTTCAAATC CTTCTTTTGG GTAAAGATTC TGAGCTCTTT GTTTGCGCTC	240
GAAGACATTT AGAGAAATAC TGTCTATATC TCTATTTTCA AATGCTAAAC TAACAAAATT	300
CCTTAAAGCC TTGCTACCTA AGCCTTGCTC CTGTTTCCTG GGGTTGATAA AAAATCTCCC	360
GATATGAAGA TTGCTGCTCT CTAGCCTGAT TTTCTGATA AATCCACAA ACTCTGTTTC	420
ATCAAGATTG GAAAGACTC CTTCCAAGGC TTGAAGTCTC AGTAGAAAAG GAATCCTTGG	480
TCCCATCCAT TGTTCTTGAA AGGATTTGCC TAGGGAGTTG GACCACTGGC ATACAAATTG	540
AGCGTTTCTT GTGCTACCTT TTTCTTCAAA ACGAATTGCT ATCTTTTCTT CACCACCTTA	600
TCTATGTTTC TCCATTATAC TATTTCTCCC ATTTTTFACG AATAGATAAG TATGATTGAT	660

1308

TTTTATTTTT TTCTCGTCGG GAGCATCTCA GCTTCCTTTC TTGGTTTGGT CATTGACCGT	720
TTTCCAGAGC AATCCATPAT CAGTTCAGCC AGTCACTGCG ATTCTCTGTCA GACTCCCTTG	780
CGTCCCTTAG ATTTGATTCG GATTCTCTCA CAGGCTTCA ATCGCTTTCG CTGTGCTAC	840
TGCAAGATTC GCTATCCTGT CTGGTATGCC CTCTTTGAAT TAAGCTTAGG ACTTCTTTT	900
CTGCTTTTACT CTGTGGGATG GCTCTCTTG GGGCAAGTGG TCCTAATCAC CGCTGGPTTG	960
ACCTTGGGTA TCTACGACTT TCACCATCAG GAATATCCCT TACTGGTCTG GATGACTTTC	1020
CAGCTAATCC TAATAGCTTC CTCTGGCTGG AATCTGGTCA TGGTCTCCTT CCTCATACTT	1080
GGAAPTTTGG CTCATTTTAT CGATATCCG ATGGGTGCAG GGGATTTCCT CTTTTAGCT	1140
TCTTGTGCTC TCGTCTTTAG CGTAACGGAG TTACTGATCT TGAATCAGTT CGCTTCTGCG	1200
ACGGGTATCC TGGCCTTTCT CCGCAAAAG AAAAAGGAAA GACTTCCTTT CGTGCCTTTC	1260
CTCTTACTTG CTACTTCTTT GATTATTTTT GGTAACTGAC TGCTTGTCTG ATAAATCCA	1320
ATTCTTGCCA TATATCCTTC ATGAATTTAT TTCACAGTTA AATATATAAT TATTTCTTTT	1380
GTACAAGGG ATGATGTTAT CAATCGATC TGTCTCTCTA TCTCTTTGAT ACTGATCAA	1440
AAATTTTCAT TCGACTGAAA ATATTTTGCT TATAAACTGT AAACGAATAC TTTGTTTAGA	1500
CATATATAGC GCTAGACTGA CTAGATGATT ACTCAAAACG ACGTCCAGAA TACTCTTTAC	1560
TTTGCTTTGGT TTTTAAACAA AAATTTGATC ATCCAAGGCT TCAATCATTT TGTAACCTTT	1620
TTGGCAATT TGACGATAAA AGTAAGAATG TTGCTTTGGA GTCAATAATC CTAACTTAAA	1680
AGCTGATAC TCTAAAGGCT GTATCGAAGC ATTCAAAATC GACTTCAATA AAATATAACT	1740
ATCAGGATTG CTGACACGGT TGCCAAACCT CTCTTCAAAAT TTGACTAAAA ACTCTTCTTT	1800
TGGCAATAAA AAACATGATG CAAAATAATT TGCTTCTTGC TCCAAACGAT CGCATCTTC	1860
ATTCATATCT TTATATTTAT GTAAAAGAAT ATGTCTTAGC TCATGAGCTA AGTCAAAATT	1920
TCGACGTACA GATGATTTAT TCGTTCCTAA CACAATATAA GGTCCTCCCA ATTTTGACCA	1980
TGCGGTATAA GCATCAGCTT GGCCATTAAAT TAATCGTTCC ACGATATAGA TGCGTGAAG	2040
TTCTAATTTA TAAAGCAAT CATGATTATC TTTTGAATA CCTAATTTTT CCCTGGCATA	2100
AAGAGCCAAT TCCTCAATGG ATTCTCCCTT ATGATAAGAT TCACCTACTA CATTAATTAG	2160
GTCAATGAAT ATAATATTAG GTATAATTAC AAAAAGTTCA AAATAATCAA TCAAACTATC	2220
TACCTATGT AAATACATAG TTGGAATATC TATTGTTTTT CGTGTGCTA GGTCTGCAAT	2280
TCTAAAGGCA ATTACAGAAG AATCAAAATG AATGCTCTCT TCTTCTGTGT CAAAATAAGT	2340
TAAATCACCA TGAATTTGTT TGGCCAAATG CATTTTGGTT GATAATTTAG GTTTCGTTTC	2400
GTTCGACTCA AACTGCCAAA TGGCTTGTTC COTTAATAAT ATTCTCTGAG CTAAATCTGC	2460

1309

TCTACTTAA CCATTAAAC GCCGTAATTC TTTCATATCC CGACCAATTAA ACATTTACAT 2520
 ACTCCTTACT ACTTTTGACC TTCTGTGTTT TCTATCTCTG GAATAATTTT AAAATCTTCT 2580
 GTTTCGGATA ATTCTGAAAA ATTAGGAATA TCTTGATATT TAGCTTCTTC GAAATGGTAC 2640
 GGG 2643

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TGACCAAGTG CAAATGGCT ATCCAAATGC AGATGTATT ATCGATGATA TCATCTCAGG 60
 GCAAGCCTAC GTAGCCTTGG AAGAGGGAAGA ACTGCTAGCC TATCCTGCTG TGACCAAGAG 120
 TCCAGAGGAG GCCTATGAAG CTATTTATGA GGGAAACTGC CAAGCTGGAG AGTCAGAGTA 180
 TCTAGTCTTT CACCGTATTG CTGTGGCAGC AGATGTGCAG GGAAAGGAG TTGCTCAAAC 240
 CTTCTTAGAG GCCTTGATTG AAGGTTTTGA TTAICTTGAT TTTCGCTCAG ATACGCATGC 300
 TGAAAAAAG GTATGCAAC ATATTTTGA AAAACTTGGT TTTAAACAAG TCGGTAAGAT 360
 GCCAGTAGAT GGCGAAGCT TGGCCTATCA AAANTAAAG AAATAATGCA AAGAAGTAT 420
 GTAAAAATCC TCTACTCTC ACCAATGGT ATTCTATCAC TTGTAGCTGA TGACCATTAT 480
 TTGTATGAA TTTGGGTTCA GGAGCAGAAG CATTTTGAGA GGGGACTAGG AGATGAAAG 540
 ATAGAAGAAG TTGTAGTCA TCCTATTTTA GACCCAGTTA TT 582

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CCCAAGCTAC TAAGAGACTA AAACCTTGCTA GAGAAGCAAG AGAAGTGTG AATCTTTTAA 60
 ATTTTCATGAT GAATTTCTCT TCTGCTACCA ATTTAGAGAA ATTTTCTCTA ACCAGCAATT 120
 CCCTAGTAT AACAAATTCA AAAAATGGAG TCAATTTATC TGCTCACGGT CCAGCAGGTA 180

1310

GCCCCGTACT TCTGAGATAA AATAGAGAGA CCTGTAAACG AACAGCAAGT CTTGAGCGTC	240
TGCCCTTTCT TCAAAATCGC TGATAAATTC TCGTAAGAA GAAACTATAT CGTAACCTGT	300
CACATCCCTT TCGTCCAAAG CCCCTGATA GTCAAGCCG GTCACTTGA GTTCCACCTG	360
AGGCAATTTT TCAGTCAGAT AACCCAAAT CCCTTGATAA TCCTTACGTT TCAAGGATCC	420
AAGAGGATT TGAGTGGAT AGCCTTCCTG CTCCTTTTCT TGTATAACT CAGCCAAGCG	480
AGTCAAGGCA GGGAGTTAT GAGCACCATC CAAATAAATC TGTGGGCGAA TACGCTCCAA	540
GCGAsCAGCC CAAT	554

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

CCGGTTTTTC AATGAATTT CTGGTGTG GCTAAAAAT ATGCTACACT ATCAATATGA	60
AAATTTTAAAT CCCAACAGCA AAAGAAATGA ACACAGACTT CCCAAGTATC GAGGCAATTC	120
CTTTAAAAAC AGAAAGTCAG GCCGTGCTTG ATGCCCTTGGC TCCTCTATCT GCCAGTCAAT	180
TGGAGAGTTT CTACAAGGTA TCAGCTGAGA AAGCGGCGGA AGAATTTCAA AATATCCAAG	240
CTTTGAAAAG GCAAACTGCT CAACACTATC CAGCCTTGAA ACTTTTGTAT GGCCTTATGT	300
ACCGCAACAT TAAGAGAGAT AAGCTGACCG AGGCGGAACA AGATTATCTT GAAAAATCATG	360
TTTTCAATTAC CTGGGCTTGG TACGGTGTGG TTCCAGTCTT GTCACCCATG GCTCCTCAAC	420
GTTTGGATT TTTGATGAAA TTAAGAGTCG CTGGTAAGAC TTTGAAGAGC CATTOGAAGG	480
CAGCCTATGA TGAACCTCTG AAGAAGGAAG AAGTGATTTT CTCTCTCTTG TCATCAGAGT	540
TTGAGACTGT ATTTTCTAAG GAAATCAGAG CAAAGATGGT GACCTTCAA TTCATGAGG	600
ATAGAGGCGG TCAGCTGAAG ATTCACTCAA CTATCTCCAA GAAAGCGCG GGGCCCTTTC	660
TAACAGCTTT AATAGAAAT CAAGTACAAA CTGTGGGGGA AGCAGCTGCG TTGAACCTTG	720
CTGATTTTGT TTACGAGAA GATTTGTAC AACCAAGGG GGATGG	766

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

COGGCCACGG TTCCATCCAA CTTACAGGT GTGCACCTGA TTGTGTATGT AATGTCTACT	60
AACGGTAGAA TTTCACCTAT CCTCCTATC TGCTCGCAGT ACCCGCAGAC TTTCGTAAAG	120
AAGAAGATAA CCTACTATAT CGTTGCTATG ATTATACTAA AGTTTCTACT TTTTGTGCAA	180
TAGATTTTAA AATTTTGGC TAATGTCTGT AATCAGGTC GGAAGTTGA CGACCTTGTG	240
ATTGCCTAGT TTTTCGCGTG CAATTTTGAG AATGGCACCT GAGTCTTTTG AAGCAAAGAG	300
GAATTTTCCT TTGCTGTAA AGACTTCGAA GTGGCGGCTG ATTTGCGTC CAGTGACATT	360
GGCTCCAATC TGATTGATAT GGCTCCAAGG AATCTGGATA AATTGTTCGA CATTGACATC	420
TGGGTAAAT TCCAAAGCCT GATCTCGAC AAGGAATTTC CCAACTTTC CAGCGATAGA	480
GAGGTAGGAA GTGCTGTGCG TACTGAGGAG TACTGTTTTG TTAAGTGATT GGGCCATGCT	540
TAGTCTTCCT TACTTTCTCC AAAAAAGCA TTGTAGAGGG CTTTAATTGC TGCTTCTCT	600
TGCTCTTAT TGACAACAAA CATAATAGAA ACTTCAC TAGCCTTGAGA CATCATCTG	660
ATGTTGATTT TGTTTTCAGA TAGAGCGCGT GTCGCAGTAG CAGTCACCTC GATATGGCTC	720
TTCAATTTTT CACCAACAAT CATAATGATA GAAAGSTCGT GTTCGATTTT TGCATGATCT	780
ACTTTAGCTT TTTGAACCAA CTGACGCAGG ATTTCTTCTT CTTGATGGG AGTTAGTTGG	840
CGAGAACGGA GAATGATAGA AAGAwCGTCG ATACCTGTTG GCATATGTTT CCAACCGATG	900
T	901

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1765 base pairs
- (B) TYP: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

CCCTGTTACG TGGATAATAG GGTAGACTG CTCAGGATTT CTAACAAAT CCACGCTTG	60
CTGCATTGGA CCCAAACCTG ATCGAAAATT CAAACCAATC CGACTATGGA GCCATTCTTC	120
TACTTCAAAC ATACACATCT CCTTGACAAA AGTCCAATCA ATTATCGCAT TAAAGTATGG	180
TTACTAATAA AAACAAGGCC AGGATTTTTC TCCCGACCTC TTACCTGGTT AGCTAATAAC	240
TAGCTACTAT GAATGTGAAT ATGGGCTAAA AACATCCACT GGAGSTCCA ACTCTTCCCC	300

1312

ATTCTCGGA GTTGGGGTAA AATGTTCAC TGGAGCTCC AACTCTTCCC CATTTCTGGG	360
AGTTGGGCTG ATACAGTCTC CCAGACTGTA TCACCTCTCC ATAAAGCTGT TGAAGACTTC	420
TTCAATCATG TTCAATTCGT CTCTGAGTC TTCTGGGATT GGTTCGAATT CGCCTTCTGT	480
TCCATCTTCG TTTTCGATGA ATGAGTAAGC TTGGGATTCA ACTTTCCTGT CTTCGTCTTC	540
TTCTGCGTTA ACTGGTACTA GAAGAACATA GTTTTACCA AATTCCTCTT TTCCATCAAT	600
TGTCAAAAGG ATTTCAAACA AGGTTTCATT TCCTTGCTCA TCTACTAGTG TGAATTAGTTC	660
ACGTCTCTCG TGGTCGTGGT TATGATCGTG TGACATAGCC TCGCCTTTAT ATTAAAATTT	720
TCTATCTAAA TAATTTTGTG AATTCAGCTG AGCTGCTAAC TTATCAATGA CTTCCTTGGG	780
CTTATTTGGA CTGATATCTG CTTGTTCAAT CAACATGCGC TCAGCAGCCA CTGTGTCAA	840
GCGTTCATCC TGATAGTCTA CTGTTAAACC AAAAACTCT TCTAGCTTTG CTCCGTAGCT	900
TGACTAGCTT CTACGGCGCG TCCACTTGTG TTGTTTCATG TTTTAGGCAA GCCCACTACA	960
AATCGTTCCA CCTGTGAAGT ATCAACCAAT TCCTTAACGC GGTCAAAACC AAATGGCGCT	1020
TGTTCTTCAT TTATCTGGAT GATTTCAGC CCTTGAGCTG TAAAMCCAAG CGATTCGCTA	1080
ATCGCCACCC CTACCGTTTT TGAACCGAGC TCCAATCCCA TAATTCCTCAT AGGTATATAGA	1140
TCGACTCCTT GTCCPTTGGG GTAGTAGCGA ACCAATTCCT CAACGATTTT ATCAGCTCA	1200
TACTTACGGA TTTGATTTTG TGCATTATTA TAACGAGGAA CGTAGGCAGG GTCTCCACTC	1260
AATAAGTAAC CTACGATTTG GTTAATTTGG TTGTAACCTT TATCGTTCAA CGAAGCATAA	1320
ACATCTGTCA AAGTTTCGCT AATTTCCTTT TTATTTGAAT CGTCCAATT AAAACGFACT	1380
GTTCCTTCAG TAAATCCCAT TCTAACACCC TCTTTCCTTA GAATAGTACC ATTATAGCAT	1440
AATTCCTTAC CTCTACAAT TCAGGCAATC TATTATTTTG GATTTCTAT TGTCTGTGCG	1500
CGCCATTTGC CAATCTATCT GAAATATATT TGCTTGGTTC ATTTTICAAA AGATTTTCCA	1560
AACCAATATT CTTCAGATGT TCCAACCTGG AAGCCTTCTT GACATCCAGA ACTTGAAAAT	1620
CAAACTAGT CGTTGTTTGA AGTTCCGTTG CGTCAATAG TTTTGTTCCT AGTTTGAAC	1680
CTGCCAATT ACAGACTTCA ATGATAGACT TATCCTTCTC CTCCGCTTCA AGAAGAGCTT	1740
TTTGAGTTTC CTCCACTCCA TGTTCG	1765

(2) INFORMATION FOR SEQ ID NO: 283:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

CTTATCCATT CACTTCTCTG TCTGTATTTC TATAAATCTT ACTCTAAGT ATACCACATT	60
TGCCCCTAGA TGTGAACGAG AGAAACGCTC TAGACATTGC CAAGAAGGAA AAAAAAGGCT	120
ACAAATGTAAC AAAATCAAGG GAGGTCTGGA ATGAAGAAAC AAAGCAAGTA CAAAGAGGTC	180
GTTTCTCTATC TGAAAATGTT TATCGAGTCT GGAAGATTTC CGACGGGTAG TCGCCTGCCT	240
TCTATCCGTC AACTGAGCCT TGACTTTCAC TGCAGCAAG ACACCATCA ACGAGCCCTG	300
CTGGAATTAC GGCACGAACA ATACCTCTAT GCCAAGCCTC AGAGTGGCTA CTATGTATTA	360
GAACAAGGGC AACATCAAGA CCTAGAAATC GAGGTTACCG ACGAACATGC CAGTGCCTAT	420
GACGATTTCC GACTCTGTGT CAATGAAACC TTGATTGGCC GAGAAUACTA CCTCTTCAAC	480
TACTATGACA ATCAAGAGG ATTAGAAGAC CTAAGACAGT CCATTACAA ACTCCTCTTT	540
GAGCAAGCTC TCTACTGCAA GGCTAACCAA CTAGTACTGA CTCTTGGAAC CCAACAAGCC	600
TTGTTTATCC TCTCTAAAT ATCCTTTCTT AGACAAGCCA AGGAAATCTT GGTGGAACAG	660
CCAACCTACC ATCGGATGAA TCGCCTCTTG ATTGCACAG GCGTGACTA TCAACGATT	720
GAACGAGGCA TTGATGGAT TGACTTGGAG GAGCTGGAAG GCCACTTCAA AACAGGAAAA	780
ATTAAGTTTT TCTACACCAT TCCCCGATT CACTATCCCG TGGGACATTC CTATTCTGAG	840
CAAGACAACG GATCATTTCT TAACCTAGCT GCCAAGTATG ATGTCTATAT CGTAGAGGAC	900
GATTATCTGG GTGATTTGGA CTCGAAGAAG GGCCAAACCT TCCACTATCT TGATACAGAG	960
GAGCCTGTCA TTTATATCAA GTCCCTCTCG ACCAGCCTTT TTCTTGCCCT TCGTATTACA	1020
GCATCTCATTC TTCCAAATGC TATCAAGAA GCATTTGTGG CCTACAAAAA TATCCTAGAC	1080
TACGACAGCA ACCTCATTAT GCAAAAGGCC CTGTCACTCT ATATTGACAG TCAATTTGTT	1140
GAAAAAAATC GTTTGGCTCG CTTGACCAAT CATGAATCTT ACCAAAAACA AATCGAGGAA	1200
AGGATAACTA AAACACCTTG TCCCCCTCCT CATTATTCCC TACACGATGG YTTATTGCTA	1260
GA CCTGAGAC AGTATCCTAA AATGCCAGT CTCAAACACA GTCAACTGGG CTTGACATTC	1320
TTTGAAGAGG CCTATTTAAG CACCTG	1346

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 900 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

CTATATTCAG AATATGCCAA AAATCGGAA TGGTATAAAT TTGCGGAGG TTCATTGAC	60
ATATTTAGAA AACTCCCCCA AAGAAATTAAT TTAAAGAAAG ATTTTCTCTAG AATTTTGGCC	120
CCCTTATTA TTAATTTGCT TAAATTAATC AATAATTATC TAGAGAAATA AGAATACGAG	180
TGGATTGACA AGAATGGAAA TATTTTTC TCCTAGTAT TTTATTAGA AGATTTAATC	240
TATCCTGGA TTGTAAACC TTTGGTTTA GAGATAAATT CATTGCCTGA AAAAGGTTA	300
CTTGAGGGG AATCGGAGCA GCACGGTAC AATATTTTTA TAACATTGTT TGACAAGGAA	360
GAGAATATAT TAAATTTTA TAACAAATAT CCGTTTAC TGAGGCAAT ATCGAGTCT	420
TGCTTCGGT TCTATACTTA TTTTATAGAA ATTTATCAA ATTTAGAAAA TGATTTTAGT	480
GTCTAGAAG AAGAAATTAG GCTAAGGGG AATTAATG ATATAAAAT TGGAAGGGT	540
GATACACACA GCCAAGGAAA AACTGTTTG ATACTCTCT TGTATGACGC GAAATTTGTT	600
TACAAGCTTA AAAATTTAAT AATCAATAA TCACTAATA CTATTGCTGA GTATATCCGA	660
AAGGTGATG AAAAATTAG GATAAGAATA CCTCGAATA TTGCTTATTC GGATCACAGC	720
TATGAAGAA TTATIGATTA TCTACCTTA GAGCAAAAGA AAAATTACC TGAATATTAT	780
TATAATTTTG GTGTGCTTT AGCATTTATA TATTATTTA ATGGGAGTGA TATACATTTT	840
GAAAATTAA TTCTCTATGG AGATATGCCT GTAATAATAG ACTTTGAAAC AATGTTACGG	900

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

TTATTAGCA GAGGCAGTT TAAATGTGAA GGATTGGTC AGTCAACAG TTTTATCA	60
GCAGATTATT GGTTAGAAA TCCTATCTCA AACGGATACA GAGGTGCTT TGGGACTTGG	120
AGGAAAAGCC TTGGTACACT TGATCAAGC ACAAGAGGT GGAGAAGTAA GGAACATTA	180
TGGTCTTTAC CATCTGGCTA TTCTTTTGGC GACACGAAAG GCTTTGGCG ATGTCTTGAA	240
GCACCTGACG GATTACAGA TTCTCTTGT TGGCGGTGCA GATCAGGTT ACAGTAGGC	300
CCTTTACTTA GAGGACTTG AGGGAATGG CATTTGAATC TATCGAGATA AGCCAGTTTC	360
CACATGGGAT ATTGAGAGG ATGACGTAT TATCGGGGTG ACTGAAGTCC TTGCGGCTCA	420
GGATATCTAT GAGTTGGGG AAAGAGTAGA GCCTTTTATC CTAGCAGAG GTACGAGAAT	480

1315

GGGCGATATT CATCTTTCTG TCAAGGATAG TCGAAAGTCC AGACAGTTTT ATCAAAACGGT 540
 GTTAGGGCTC GAGGATAAAT TCACTGTGCC TAGTGCTAGT TGGATCGCAG CTGGGGACTA 600
 CCATCATCAT TTAGCACTCA ACGAATGGGG AGGAAAAGGT CTGGATCCGC GTAAACAAGT 660
 CCTACCAGGT TTAGCCTACT ATGTCATCGA AGTCGCACAT AAGAAGAAGC TGTTAACGAT 720
 TGCCCAACGA GCACAAGAAG TTGACCCACC AATCAAAATGG ATGACATCGA TCCAATTGGA 780
 AATCAGAGAC TCAGATGGCA TCGTGACCCG TATTCGTTTA GCTAGATAGA TGGTATGTGA 840
 TGAAGGTAGA GCATCAATPG TA 862

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

TCGTTTACAA GATCGCTAAA ATGCATCTCA TGATCCGGAC CACGAATTCC AAGATAGCAC 60
 GCGCTACCTC AATCATAGAT AGTTCACTTT TTTCTTGCCC AGCAAAATAC TCTAATTCCA 120
 AAGCGTTTCT CCTCATTTAT ACTACTATCG CCAGAGCGAA CAGACTCTGA CCTCATTTTA 180
 TCAATTTACTC TTTATTTTAC GATAATTTTG CGGAATAGTC AAAGGTTAAG GGGAGAAAG 240
 TGGCAGGATT AGACTAATTC CAATATAAAA CTCATTCCCTT TTTCTGTGC TCCATTTTCC 300
 ACAATCCAA GCGACTTGAA ACACCTCCTA GAAGCATGAT GTAGGTGTA GATTTTCTTG 360
 ACTCTCAATT CTTTCCATCC TTTTACTCGA GCCAATTCAA TCAAAGCACT TAGAATCTTT 420
 TTTCCAAATC CTCGATGTTG GTAAGCGGAA TTCCCAATCA CAATGGGGAG ATTATCCTGA 480
 GATAGTGTA TATCCCAAT TGGAACCAT TCTCCCTTCT CCTTGACTTC AATCCAAAAA 540
 AGCTCCACAT GCGATyCAR ATAGGAATAC ATGGCTTCCA AGGTCGctG ACTGTAAGGA 600
 AGCTTCACCC CATCTACGAG GTAAcCAAGT TCACATCCGT GATACCAAGC 650

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

1316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

GATAGCAGATC CGCTTCAGAA ACTTCTCGCT TACCTCTAAC TCCGATCGCT AGTTTGGGAG	60
AAGATACATTC CAITCTCATA CTATCTGTGT GCTTTGCAGG CTGTAAAAAC AACTTTTCTC	120
TTGCTACTTC CTGAAAACT GAATCTTGCA GTTCTTGCT TTCAAAATAG TCTGTACTC	180
GCTCCACATC AAAAATCCCA GCTAAAGACA GAGACATGTT TACAGGTTTG TAAAACCTTG	240
TAAAATTTTC TTGCAAAATTA GTTAGATTGA TTGGGAAAT GGACTCCTCA CTTCCAACTA	300
TATCAGTTGC TAAAGGTGTA CCAGGATACA AATTGCTAA AGTTGAAAAG AATAAACACG	360
AATCTGGATC ATCTTGGTAC ATTTCTGTT CTGTGTAAT AATATCTGTC TCTGTACGAA	420
TGGAGCTTC AGTAAAGTGT GCTGATGTTA CCAATTATC AAGTAAATCT AAATTTTCTA	480
AAAAATAATC CGTTGCTGAA AAAAGATAGT TTGTTTTGT AAAGCTGTA AAGGCATTAC	540
TATCTGCACC TAGACTCGTA AAGCCGACA TCAATCACT AGAATCTCT CTCTCAATA	600
ATTTATGTTT AAGAAAATGA GCAATTCCTC CAGGATATTG TTTTACATCT CCGTCAACTT	660
CTGTGACAAA CGTATCTACC GAACCAAACT GTACAGTGAC ACTCCGTAA ACCTCTTTAA	720
ATTCCTTTTT AGGCAAAAAG GCAACTGTCA ATCCGTGGC CAAACGAGTT CGATAAACCA	780
TTTCTTTTAC AGCTGGATAG TATTTTCTT CAAAAACAAC CTTTGTCAAT CTATTCCTTC	840
CATAAGTAA ATCGCTTGTA GTTTCACATT ATTAGTACT CTACAAATAG CATCTTTGTC	900
AATTTGTCA AGCTTTGCAA TCCAACTTT AAAGCTGCT GAAGATTTTC CAAATAAGGC	960
ATTTGTGATA GCACGTTCAA TCAATGAAGA ATGATTATCT TGAGAAAGTA ACAACGACCA	1020
ACGAATCATT TCCTTGGTCT GATTTAACTC AAACCTGTGA AAAAAACCTT TTTTAAATC	1080
AAGCGGTGA TTATTCATCA ATTACGAGC CTGGTTACG	1119

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ACGCCCTGCG GGGACATGA CGAATTCCCC GTTCATCAG AAGCCGCCG AGGAGTGGGG	60
GGTGCCGTC AAGTCAAAAG CGGCCCCACA TCGATTCAAT TCCCGACGA ACAGCCCTTT	120
CCCCAGCGT TCTGGCTTT GCAACCGTTT CACAACAGCC TCGTAAAGTA GGCCGACAA	180
GCGACAGCA CTCCAAGGA GTTCTTCCAT CTGCAAGTGC GCCTGCGTTA TGTGATCCCG	240

1317

GTCTTTTGCA TGTGTGTGGC ATGAATGCTG TTCCCAATCC CACTCCAGAA CATCTCTCTC 300
 AAAAGTCGCG AACGTGCGCC TGAATGAATC CTGCCTTGTA GTCGTAGCCA TTCTATGAA 360
 GGGTCGCAGA GGATTTTCCC CGAGTGCAGC CGCATCCTCC GGCTCAAAATC GGGTGCATTT 420
 CACAGTCCCG CTCAACGCTA GCCCGATCCC TTTTTCGCAT GGTGACTCAA GCGTCTTTTC 480
 AAACAAAAGC TCCTCATCCG CTCCAACCGC CCGACGTAG ACCTGTAGAC CGAAGTCGTC 540

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1949 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AAAGAAATTCG ACCAATTCAA GGTGTAGGCA TCGCAAACTA TGGACTGTTC CCCCGTCAGT 60
 TCTGGACAGA AAACGGGATA AGGTGTGCTG TGAAGCAAGC TGCCCTCCTA CCAACAATTT 120
 TGGAAAGTAG GCATCAGCTG ACAATTCCTT ACAGCATAG TCCGTTCCAT AACCTGTTAA 180
 CAGTTGAJAG AGGAAGTGA CAAGGATATC TGAATCCGAA TAACGACAGT AGCGGCGTTG 240
 GTCATTCGTT ACTAAATACT TAGAAATCCG CTCCTTTAGT TTCAACTGGG AAAAAGTTTC 300
 CTGAAAAAAG ATAAGACCAC CATACTGGGT TAANTGACCT CCATCGAAAG ATAGTTGGTA 360
 AAAAGACTTG TTTTGAAGT GATGATTTGG TAAACTGTTC ATGTGAGTTT CCTTCTTTTT 420
 TGTGTTTTTT TCTACACTTA TACCATAAAG GGGAACTCT TTTTGTGCTA GTAAAAAACA 480
 CCCATTGGGT GAAAAAAGAA ACCATCCAGG ATCTAAGCTA AGGCAAGGAT TCTGGATGTT 540
 TTTTGAATTT GGGGTGAATA ATTGGGGTTT TACAATATCA ACTCCCATGA TAGTCATGAG 600
 ATGACTCTTC ACGAATTGAC GTGATGACTG TCCTTCCTTT TGCAATAATTA CCTCGAAAC 660
 ACAAAAAAAG GGGTAGACAA TCTAGTGTCT ACCCCGAAJ JGTTTATTAA ACAAAAAATCC 720
 TGCCAAJAGAA TTTTGGCAG JAAJACCAAT CAATTTATCA GTTTCTATCA ATGCTTATC 780
 GCTCTCAJAG ACTGTAAAT AGGGATTCG CAATCAAAAT GCGATACTCT ATTATTAAAG 840
 AGTAACTGAA GCTCCAGCTT CTTCCAATTT AGCTTTGATT TCTTCAGCTT CTGCAJTTGC 900
 AACGCTTCT TTAACAAGTG CTGCTGACCC GTCAACAAGT TCTTTAGCTT CTTTAAGACC 960
 AAGACCAJTG ATTTACAGTA CACTTTGAT AACGCCAAT TTTTGTGCG CTGCAJATGT 1020
 CAATTCAAGC TCGAATGAAT CTTTAGCAGC ACCAGCATCA GCTGCATCAG CTGCAJCAAC 1080

1318

AGCTACAGGA GCAGCTGCAG TTACACCAAA TTCTCTCTCG ATAGCTTTTA CAAGTCGTT	1140
CAATTCAAGG ATTGAAGCTT CTTTAATTTC AGCAATANTG TTTTCAATGT TCATGCGAT	1200
TGTTATTTCC TCCAAATAAG TTTTAAATTT TATAATAGTT TTTTTCGTAG CTAGksTACG	1260
CTGTGTAGCT TAAGATTAAAG CCGCCTCTTC TTTCCTTTCT GCAACCGCTT TGACTGCAAG	1320
AGCAACGTTG CGCACTGGCG CTGGAAGTAC AGAAAGAGC ATAGAAAGAA GTCTTCGCG	1380
GTTTGAAGA GTTGCAAGTG CAAGAATCTC TTCTTTAGAT GCGACAGCGC CTTCGATTGC	1440
ACCACCTTTA ATTTCAAGTG CTTCAGCGTT TTTAGAAAAG TCGTTCAAGA TTTTCGCTGG	1500
TGCGATAACA TCCTCATTAG AAAATGCTAC TGCAGATGT CCAACAAATA CAGATGCAAG	1560
ATCTTCAAGA CCAGCTTTTT CAGCTGCAGC AGCAAGATT GAGTTTTTAA TAACTTTATA	1620
CTCAACTTCG CTTCCAGGAA GCTCAGCAGC AAGAACTGTA TCTTGCTCAA CTGTCAAACC	1680
ACGAGCGTCT ACAACGACGA TAGATGCAGC AGCTTTTCATT TTTTCAGCTA TACGTCAACT	1740
AGTTCCGCTT TTTTAGCAAT AATTGCTTCA CTCATATAGT GTTTCACCTC CGTAATTATT	1800
TTGCTTGGGG AATTTTTCAA AAGAAAAAC GCGCCCAATC CTAGACACGA AAGTACAATA	1860
CGCTTCTTTT TACATGATAC GTTTTGTGCT CGGTAGGATA TTTATGAGTC GAGCTCCCTT	1920
ACTGTCTTAG GCAGTTTTTT TAGATACGG	1949

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1023 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

GGACTGTTTG ATCTTATACA GTAGCTGCTT GATCCAAGCT TTCACCGATA GCGGCTAGGC	60
GCTCGATAAC TTCAAGCTGT GTCAATTCAAT TTTTGAAGC ATAGCGGTTA CGTGGGTGA	120
CACGGCACTC GTGTGAGCAT CCACGAAGGT ACTTGTCTTC ATTTCTTCTT GATGTCAAGA	180
TACGACGGTT ACAGATGGA TTTCCACAGT TGACATAAGC TTCACATGGT GTTCCATCAA	240
ACCACTCTTT CCTACGATA GTTGGGTGA CATGGTTGAC ATCAACGGCA ATACGCTCGT	300
CAAAGACGTA CATTTTCCCA TCCCRAAGCT CACCTTGAAC TTCTGGGTCT TTACGTAAAG	360
TTGGCATTCG TCCGTGCAAT TGGCGGACAT CTTTGTAGCC TTACCGGACC ATCCAGCCTG	420
AGAATTTCTC ACAGCGAAGC CCACCTGTAC AGTAACCAC GACACGCTTG TCCATGAATT	480
TTTCTTGTTT ATCAGCGACC CATTTGTGTA ACTACGGAA GTTCGGAATA TCTGGGCGAA	540

1319

TAGTCCACG GAAATGTCCT AGGTGCTACT CATAATCGTT ACGTGTGCA AGGACAACGG 600
 TATCTTTATC AAGAAGCGCT TCTTGAACCT CTTTGGAGA CAAGTAAGCA CCTGTTGTTT 660
 CAAGTGGGTT GATGTCATTG TCAAAGTCGT TGTCTTCCAA ACCAAGGTGG ACAATTTCTT 720
 TCTGTGAGCG AACAAACATC TTCTTGAAGG CTGTTCATT TTCTTCGTCA ATCTTGAACC 780
 AGAGTCTTTC CMTTCCGGA AGGCTGTGAA CGTAGTCCAT GTATTTTGA GTTGTTCAT 840
 AGTCACCTGA AACTGTTCCG TTAATTCCTT CGTCAGCGAC TAGGATACCG CCTTTAAGGn 900
 CSATFGATTT ACAGAAAGCC AAGTGGTCTG CAGCAAAATG CTCTGCATTT TCAATTGGAG 960
 TATAAAGGTA GTAAAGTAAG ACACGAATAT CTTTgkCaw AAGATTTGTA TCTCTTTATC 1020
 TAT 1023

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3831 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

ACTATGAACA AGACCCAGAA AAAGTAGCCT TATTCTTAA GAATTTTAAT AGTTTAAAGC 60
 ACCTAGACCC TGTTTAGATT GACGAAACAG GATTGATAC TTATTTTAT CGAGAATATG 120
 GTCGCTCATT AAAAGGTCAA TTAATAAGAG GCAAAGTATC TGGAGAAGA TATCAGAGGA 180
 TTTCTTTGTT TGCAGGTCTA ACAATGGTG AATTAAATCG TCCANTGACT TACGAAGAGA 240
 CGATGACGAG CGACTTTTTT GAAGCTTGGT TTCAGAAATT TCTCTTACCA ACATTAACA 300
 CACCATCGGT TATTATTATG GATAATGTAA GATTCATAG AATGGGGAAG CTAGAACTTT 360
 TATGCGAAGA GTTTGGGCAT AAACCTTTAC CTCTTCCTCC CTACTCGCCT GAGTACAAATC 420
 CTATTGAGAA AACATGGGCT CATATCAAAA AGCACCTCAA AAAGTATTA CCAAGTTGCA 480
 ATACCTTTTA CGAGGCTTTT TTATCCTGCT CTTGTTTCAA TTGACTATAT TAGAGGGGAG 540
 ACATTTTTCG GTTCTTTGTC AACTGTAGTG GGTGAAGAA AGCGAGATC TAGAAAGGAC 600
 AAATTTCGTC CTTTCTTTT TGAAGTTTC AAGTTCTTA AAACCAAAGG CATTTGCTTT 660
 GATAAGTTTG ATGAGATTAT TGGTGGCTTC CAGTTTGGCG TTGGAATAAG GTAAATTGAAG 720
 GCGGTTGACG ATTTTCTCTT TATCTTTGAG GAAGGTTTTA AACAAAGTCT GAAACAGAGG 780
 TGGAAAGACA AGAGCTGATA GAGATTATAG TGGTGTTTAA AGTCTTCGGA ATAGCTCAAA 840

1320

AGTTTATCTA GAATTTCTTT ATTAGTCAAG TGCATACGAA AAGTAGGGCG ATAAATCGT	900
TIATCACTCA GTTTCGACT ATCTTGTTGA ATGAGCTTCC AGTAGCGCTT GATAGCCTTG	950
TATTCATGGG ATTTCCGATG ATGGCTTGTC TCTGCTCTC AAGAACAGTT ATGATATTGA	1020
GTTTATCAAA GTCCGAGCA ATAAAGCTCA TCTCCATCTC CCGATTGAAA CAGTCACTCC	1080
CCGGCACTGT TCAACCTCTT AGGCATATAT TCTCAGAGAA CCGGAAAAAT CATGCTCAAA	1140
GTGAAATCA TTGTCTTGC GAATGACAGT TGAAGTTGAA ATAGACAACT GATGATCAAT	1200
GTCCGTGATA GAACTCTTTT TAATTAGCTT CTGAGCAATC TTTTGCTTGA TGATACAAGG	1260
AATTTGATGA TTCTTCTTGA CGATAGAAGT CTCAGCGAGC TCCATTTTTG AGCAATGATA	1320
GCACCTAAAA CGGCCCTTTT TAAGAAGAAT TCTAGTTTGA ATTTTTTTAT ACTAGAAAA	1380
CAGAACCATA ATACCTATAT AAAAATATTA TAGTTCTAAT AGGATTTACC CAAAAGTTTT	1440
AAGCGGCTCT TTTTAGAACT TTAATTGTTT GAAATTAGG TAGCAAAATT GTTTCATATT	1500
TGTCACTGTT TCTATTTTT ATCTTGTTGA GGTGCTATT TTAACAATTC AGGAATTGAT	1560
AGTGAATGTG TAAATTTTT TGTAGAATA AGTTTATATA AAGAAAAAGG AGTATTGAT	1620
TATGTTACAA AAAATTTATG AGCAGATGCG TAATTTCTAT GATAGTATTG AAGAAGAGTA	1680
TGCTCTTACA TTTGGTGATA ATTTTGACTG GGAACATGTT CATTTTAAAT TTTTAAATTA	1740
TIATTTAATG AGATATGGCA TTGCTTGCTG TAAGGATTTT ATTGTTTACC ATTAACGCTG	1800
TGCTTATCGT TTGTATCTTG AAAAATGGT AATGAATCGG GGTTTTATTT CTGTTGAGG	1860
TAATTTTAGT AAATTTCCGA ACTAATTTAC TCTTTTATGG AAGATGATA GTAAATAGCT	1920
AGTAATTTTT CTAAATCATT TTTTAATAGT TCGAAATAGC AAATCTTTCT ATTGTTTCTT	1980
CTTGATAAAA AGGCGATTTT TTATTTAAT AAATTTGTAAG ATATAATTGC AGGTGAGAGT	2040
CCTGCCATGT ATGTGAGAAA GGAAGAGCCT GATGGCTCAG ACAAGATTAT GACTTCAGTT	2100
GTTGTTGTAG GTACCCCAATG GGGTGATGAA GGTAAAGGGA AGATTACAGA CTTCCTTTCA	2160
GCGAATCGAG AAGTGATTGC ACGTTACCAA GGTGGTGATA ATGCTGTGCA CACGATTGTC	2220
ATTGACGGTA AGAAATTTAA GTTGCACTTG ATTCCATCTG GGATTTTCTT CCCTGAAAAA	2280
ATATCTGTCA TTGGGAATGG TATGGTTGTA AATCTTAAT CTCTTGTAAG AGAGTTGAGC	2340
TATCTTCATG AGGAAGGTGT AACAACTGAT AACTTGCOTA TTCTGATCG TGCGCATGTT	2400
ATTTGCGCTT ATCATATCGA GTTGGATCGC TTGCAAGAG AAGCTAAGG CGACAATAAG	2460
ATTGCTACGA CAATTAAAGG AATTGGTCCA GCTTATATGG ACAAGGCTGC TCGTGTGGA	2520
ATTGCTATG CAGATCTTTT AGATAAAGAT ATTTTCCGTG AGCGTTTGA ACGTAACCTT	2580
GCTGAAAGGA ATCGCTTTTT TGAATAATTG TATGACAGTA AAGCGATTGT TTTGATGAT	2640

1321

ATTTTGAAG AATATTACGA ATATGGTCAA CAAATCAAGA AATACGTGAT AGATACATCT 2700
 GTTATCTTGA ATGATCGGCT TGATAATGCC AAACGTGTCG TTTTGAAGG TGCACAAGGT 2760
 GTTATGCTAG ATATCGACCA AGGTACTTAT CCATTGTGTA CGTCATCAAA CCCTGTAGCT 2820
 GGTGGGTGTA CAATTGGTTC TGGTGTGGT CCAAGCAAGA TTGACAAGGT TGTAGTGTGA 2880
 TGTAAAGCTT ATACGAGTCG TGTAGGAGAT GTTCCTTTCC CAACTGAGTT GTTTGATGAA 2940
 GTGGGAGAAC GTATCCGTGA AGTGGGTGAT GAATATGGTA CAACAACCTGG TCGTCCACGT 3000
 CGTGTAGGTT GGTTCGACTC AGTGTGTATG CGTCATAGCC GTCGTGTTTC TGGTATTACT 3060
 AACCTTTCTT TGAACCTCAT TGATGTCTTG AGCGGTTTGG ATACTGTGAA AATCTGTGTG 3120
 GCCTATGATC TTGACGTGCA ACGTATTGAC TACTATCCAG CTAGTCTTGA ACAATTGAAA 3180
 CGTTGCAAGC CTATCTATGA AGAGTTGCCA GGTGTGTGAG AAGATATPAC CGGAGTTCGC 3240
 AATTGGAAG ATCTCTCTGA GAATGCGCGT AACTATGTTC GTCGTGTGAG TGAATGCTGT 3300
 GCGCTTCGTA TTCTACTCTT CTCAGTAGGT CCTGTCGTG AACAAACAAA TATTTTAGAA 3360
 AGTGTTTGTT CCTAAGAGAT TTTTAAGATT TGTTAAGAT AGTCTGGGTA TACTATAGAC 3420
 GGTACAAAGA AGACCTCCTA ACTTGTGTGA ACAAATATTC TAAACTTTTC TTTTTCATAA 3480
 TAATCTCCCT ATAGAGTCAC CGCATTCGTT GCCTTTTTTT GTGTTGGGAT TCATGATATA 3540
 ATAATAAAAT CGATAAGTAG GAAAAGAGAA AAGAGATGTA TTATACGCTT GAAGAAAAAG 3600
 AAGTCTTTAT GAGGGAGGCT TTGAGAGAGG CTGAGATTGC TCTTGACAC GATGAAMTTC 3660
 CAATTGGTTG TGTGATTGTC AAAGATGGGG AATCATTTGG TCGTGGGCAT AATGCGCGTG 3720
 AGGAATTACA GCGAGCGGTT ATGCATGCGG AATTTATGGC TATAGAGGAT GCGAACTTGA 3780
 GTGAGGAGAG TCGCTTTGCT GGATTGCACA CTTTTGTGA CCATTGAACC G 3831

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1441 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CCGCTGTTC AACCGAACA TACCATAGTC CGTACGGGAT TCGAACCCGT GTTACCGCG 60
 TGAAGAGGCG GATGACTTAA CCCCTTGACC AACGACCTG AGTTGTTATT TTCACTCTT 120
 ACTATTATAC AGTCTTTTCA AACTTTGTCA ACTACTTTTT CTAATTTTGG TTATATTTTT 180

1322

CAACTTATAG TAAAAAAGC CAGAAITATA CTGACTCTTC TATCGCTCAT TAAACTTAGA	240
AGCAGCTTCT TTTCGCCACC AATAAGGGAT TAGTTCTGCG ACTTTAACTG TTTTCTTAT	300
ATTATAGTCC ATCATGAATT CTGCATCTTT ATTTTCAGCA TTAAGCTCTA AAAGGAATTC	360
TCTACAAGCA CGCAGAGCA TGGCTGAAC TCCACCATAA GGTGTTTGT CTCGAAAGCC	420
TAATACTTTC TTAACCTTAG TTTGTCCTGA AAATTGGTAC ATATTGAAGA GGGCCGCCG	480
TTCTGCGCAG AGATGGAAAA CACCACAGGT TCCCTCCATA CAGAACTCTG TAAATATTGT	540
TCCATCTCCT GCTTCTACTG CAGCTACAAC ATGATTGGCA TAAACAAAGT CTGATACTTC	600
ATGTGGATTG TATAGTTTCT GTGCTTCTTC GTACATCTTF TCCCAGATGT CCATTATTGT	660
ATCCTCTTTA TTTAGAGATT TCTTTTAGCA TGTTTTCGAT ATGCTGAANT GATTTTTCAC	720
GTCCAAGCAA GAAATTTGTA TCTGGTAATT CTGGCCCATG CATTTGCGCT GAAACTCGA	780
TACGAATAGG CATGAAGA TTTTCCCTT TAATACCTGT TCTTTTGGG ACTGCTTTAA	840
TTTGTGGGAA GATATTTTCT GTCACAAAAT CATCATCTGT CATCGCTTCA AGTTTTCCTT	900
TGAATGCTTC AAGAACTGTT GGAAGTGT TACCCTGCAT GACTTCGCGC TCTGCTTCTG	960
TCAATCTCGG GAAATCTGAG AAGAAAAGAT CTGTCAATGG GATAATCTCA TCTACTGATT	1020
TCAATTTGGG TTATAGAGC TCAACTAATT TTTACGCTT GTCACTCAA CGGCTGCTT	1080
CCTCTAAGAA TGGTTTGGC ATTTCAAAGA TGGTTTCAAG GTCTGCATTC TTGATATAAT	1140
CATGTCTCAT CCAGTCTAGT TTTTCTGAT CAAAGGCTGC TGGTGACTTG CTGAGCGGT	1200
TTTCATCAA AAGTTTAATG AATTCTTAC GAGAGAAAA CTCAATCCCA CCACCTGGT	1260
TCCAACCAAG AAGAGCAATA AAGTTAAAGA CTGCTCTGG AAGGTAACTT TTCTTTGGT	1320
AATCTTCGAT AATTGAAAT GTATTAGTAT CACGTTTAGA TAACTTCTTA CCAGTTTCAG	1380
AGTTGATAAT CAAGTGTCAT GTGACCGAAC TCTGGAGCTT CCTCAACCTA AGAGCGGTA	1440
T	1441

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

CGGCTTATGT AGTGGAATC TTTCTACGTA AGCGAAACGA GGGGAGATTA CAGGCGCTAG	60
AAGAAAAAAA AGAAGAACTA TACAATCTTC CAGTAATGA TGAAGTAGAA GCTGTAAJJA	120

ATATGCACTT GATTGGACAA AGTCAAGTGG CTTTCCGTGA ATGGAATCAA AAATGGGTGG	180
ATTATCTCT CAACTCTTTT GCCGATATG AAAATAATCT CTTTGAAGCA GAAGGCTATA	240
ACCATTCATT TCGTTTCTC AAGGCCAGTC ATCAAATTGA CCAAAATTGAG AGTCAAATTA	300
CTTTGATTGA AGAAGATAT GCGGCAATTC GCAATGCTTT GCGAGACTTA GAGAAGCAAG	360
AATCTAAAAA TAGTGGTGGT GTTCTTCATG CTTTGGATTT ATTTGAGGAA CTTCAGCATA	420
GAGTTGCTGA AAATTCAGAA CAGTATGGTC AAGCCTTGGG TGAAATTGAA AAACAATTAG	480
AAAATATCCA ATCTGAATTT TCACAAATTG TAACCTTGAA TTCATCGGGT GACCTGTGG	540
AAGCCGAGT GATTTTGGAT AATACAGAAA ATCACATTTT GGCCTTAAGT CATATGTGG	600
ATCGTGTCC AGCCTTGGTT ACGACGCTTT CTACAGAAAT GCCAGATCAA TTACAGGATT	660
TGGAAGCCGG TTATGCTAAA CTAATTGATG CTAATTATCA TTTTGTGAA ACGGATATTG	720
AAGCGGTTTT CCACTTGCTT TATGAAGCAT TCAAGAAAA CCAAGAGAA ATTCGTCACT	780
TGGAATTGGA TAATGCCGAA TATGAGAAAT GACAGCACA AGAGGAAATC AATGCTTGT	840
ATGATATTTT TACTCGAGAA ATTGCTGCTC AGAAAGTAGT GGAAATCTA CTTGCAATCT	900
TTCCAACCTA TCTTCAACAT ATGAAAGAGA ATAAATCTTT ATTTGGGAGAA GATATTGCAC	960
GTTTGAACAA GACCTATTTA CTTCTTGAGA CAGCTGCAAG CCATGTTGGT CGTATTGAGA	1020
CAGAATTAGA GAGTTTGGAG GCAGCTATTG TTGAGGTAAC TTCAAATCAA GAAGAACCAG	1080
CCTAAGCTTA TTCAGTTCTT GAAGAAAATC TTGAGGATTT ACAAACTCAA CTAAAAGATA	1140
TTGAAGATGA GCAAAATTCA GTTAGTGAGC GCTTGACACA AATTGAGAAA GATGATATTA	1200
ATGCACGTCA AAAGGCCAAT GTTTATGTCA ATCTCTCCA TACTATCAAG CGATACATGG	1260
AAAAACGCAA TCTGCCAGGT ATTCCACAAA CTTTCTTGAA GTTATCTTTT ACGGCAAGCA	1320
ATAATACCGA GGATTTAATG GTTGAGTTAG AACAAAAAT GATTAACTTT GAATCTGTTA	1380
CCCGAGTTCT TGAAATTGCA ACGAATGATA TGGAGCTTT AGAAAACGAA ACTTATAATA	1440
TTGTACAATA TGCAACTTTG ACAGAGCAAC TCTTGCAATA TTCTAACCG TATCGCTCAT	1500
TTGATGAACG CATTCAGAA GCATTTAACG AAGCTTTAGA TATTTTGAAG AAAGAATTG	1560
ATTATCACGC TTCAATTGAC AAGATTTCTC AAGCATGGA AGTGGCAGAG CCGTGTGTAA	1620
CCAAATCGCT TGTTAACCTA TATGAGAAAA CACGTGAAAC GATTGTTTTT TAATAAAAGA	1680
AAAAGATTTT ATTTGTGTGAG GAGCAGAAAT AAATCTTTTT CTATAGTTGT GGGGAGATTT	1740
ACTTCATTTT CTCCTGAGAT TGAGTTTGTG CCCAGCCGAT TTATCCACTA CCTCAAAACA	1800
GTGTTTATTA CTCTTCGAAA ATCTTTTCAA ATCACGTCAG CGTCGCTTA CCGTACTCAA	1860

1324	
GTACAGCCTG AGGCTAGCTT CTTAGTTTGC TTTTGTATTT TCATTTAGTA TTAAAGTGAT	1920
TTCCGCAGTCT TTATCTGCAG CTTCAAATCT GTACTTTGAG TAACCTGGTA ACCGTCCAA	1980
AACGAAGTCT ATTGAAAAAT CTCCAGACTA GAGAACTCAC GGATAGTTCC TAATCTGGAG	2040
ATTTCTTATT TGCACCTTTC TTGTACAAC TTAGTCCACG GFAAATAGAC CTCTAAAAACC	2100
TCTTTGTGTTA CGAGAGTTTC CTCGTTTGGG AGACATCTTA GAAGATAGGA TAGATATTTC	2160
TCGCTATTGTA TACTAGACTA AAATCAAAAA GCATTATATA ATAGTGATAT GAAATCAACT	2220
AAAGAAGAAA TCCAAACCAT CAAAACACTT TTAAAAAGCT CTCGTACAGC TAAATATCAT	2280
AAACGCCCTC AAATCGTTCT ATAGTAAAA TGAATAAGAA CAGTACAAAT CGATCAGGAC	2340
AGTCAAATTG ATTTCTAACA ATGTTTTAGA AGTAGAGGTG TACTATTCTA GTTTCAACTC	2400
ATTATATTTC GTCTGATGGG CAAATCTTAT AAAGAGATTA TAGAACTTTT ATAGTAGATT	2460
GAATTAAGAT GTGAACAAC CTATCAGGAA AGTCAAAATA ATTTATAGAA ATATTTTAGC	2520
AGCCAAGGTC TACTGTTATA GATTCAATAC ACTATAGACT GTAATCAAAC AACGATTGGG	2580
CGAAATGTAA AAAAAATAGA GGAGTTTGGG CTCGACTCTC TCCTTCAAGA AACACGTGGT	2640
GGTCGTAAAC ATGCATATAT GACAGTTGAG GAAAGAAGG TCTTCTTTCG CCGCCATTGG	2700
AAGGCTGCAG AGGCAGGAGA ATTTGTTACA ATTGATGCC TATTTTCAGC TTATAAAAAG	2760
GAGTTAGGTC GTTCTACAC ACGTGATGCC TTCTATCAAC TGTGGAAGTG CCATGTTTGG	2820
CGAAATATTA TGCCACGTCC AGAACATCCT AAGAAAGCAG ACGTCAAAAC CATTTGTCGC	2880
TCTAAAAATA AAATCTCAAT TCAAGAAGAA AAGAAAGCGC TTTAAAACCA GTAGACGTTT	2940
TCGTAAAGTT CGCTTGATGT ACCAAGATGA GSCGTGTTTC GGTAGAATCA GTAAACTGGG	3000
ATCTTGTGGG GCTCCAATAG GAGTAGGTCC ACATATCCAT AGTCACTATA TACGAGAATT	3060
TCGCTATTGT TATGGAGCTG TTGATGCCCA TACAGGCGAA TCATTTTCT TAATAGCTGG	3120
TAGATGTAAT ACTGAGTGA TGAACGCTT TTTGAAGAG CTTTCACAG CTTATCCAGA	3180
TGATTATCTT TTACTGTTA TGGACAATGC TATATGCCAT AAATCAAGTA CCTTAAAGAT	3240
TCCGACTAAT ATTTGGTTTA CCTTTATTCC TCATACACA CCAGAGATGA ACCCCATTGA	3300
ACAAGTGTGG AAAGAGATTG GTAAACGTGG ATTTAAGAAT AAAGCCTTTC AAATTTTGGG	3360
AGATGTCATG AATCAACTCC AAGATGTTAT ACAAGGATTG GAGAAGGAGG TGATAAAGTG	3420
CATCGTTAAT CGGAGATGGA CTGAATGCT TTTTGAAAC AGATGAGTAT AAAAAGAAAG	3480
TCCTCATTTT AATAGAAATC ACGACTTTCT GATGGATTTA TAGTAAAAAG AAATAAGAAC	3540
AGACAAATC GATCAGGACA GTCAAAATGA TTTCTAACAA TGTTTTAGAA GCAGAGGTGT	3600
ACTATCTAG TTTCAATCTA CTATATTTTT GAGTGATAG AAAAGCCCTT CATAGCTAG	3660

1325

TCCTACTTGT	CAGSTGCGAG	AGCTTTGACA	TCCTTTCTCTG	TACTTAGCCA	AGTCAGTTTT	3720
CCGTTCTCAA	AGCCTTTATA	TAGTAGCCAA	AATCCTTGAC	CATCCCAGTA	AAGGGCTTTA	3780
AAGCGGTCTT	TACGTCCACC	ACAAAAGAGA	AAGACTTGAC	CGGAGAAAGA	ATCCAATTCA	3840
AAGTGGGTTT	TAACTACATA	GGCTAATGAG	TCTATTCCTT	GCCTCATATC	TGTCTTGCCA	3900
CAACAAGGT	GAACCTGACC	TAAATCACTT	AGTTGAATTA	TCATAGTACA	ATACCTTTCC	3960
TCCGATAATT	ATTTTTTATC	TAGTATACCTG	GAAGTTGGGG	AATTAGGATA	GATACCTTGT	4020
TATGACGCGC	TTACGTAAC	TGTAACCTAGC	TGCCTAGTTT	GATCTTTGCT	TCTTCATTGA	4080
TTAGCAGTAG	ATTTCAAAAT	GATAAAAACG	CATAGTATCA	GGTATTGAAA	TGTAAGTGGC	4140
CAAAAGTTAG	ACAGAAAAAA	CTTAACCTTT	GGGGTGTCTT	TGTTATGAAA	TTAAGTTATG	4200
ATGATAAAGT	TCAGATCTAT	GAACCTTAGAA	AACAAGGATA	TAGCTTAGAG	AAGCTTTCAA	4260
ATAAATTGG	GATAAAATAT	TCTAATCTTA	GGTATATGAT	TAAATTGATT	GATCGTTACG	4320
GAATAGAGTT	CGTCAAAAAA	GGAAAAAATC	GTTACTATTT	TCCTGATTTA	AAACAAGAAA	4380
TGATTAATAA	AGTCTTAC					4398

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AGATTTT	TAG	ACTTTGCTT	TAATCGTTT	TTTTTAGGGA	TGATTGCGAC	ACCTCTTTTT	60
GGCTATT	TAA	TTTAGCAGGA	GGGATTATCC	TTGGCTTAGC	GCCGGCTAGT	GCCACCTTGA	120
TGAGCTT	TATA	TGCAGAACAT	GTTATAGCT	TTCCGGGAATA	CAGTTTGAAG	GAGGCTTGCT	180
CTCTTT	TACAA	GCAAAATTTT	GTCTCAGCA	ACCTGATTTT	CTATAGCTTT	TTAGGTGTGG	240
GTCTAG	TTTT	GACCTATGCT	TTGTATCTCT	TGGTGCAAT	GCCTCATCAG	ACCATTTGTC	300
ATTTGAT	TGC	GACCTTTTG	AATGTCCTAG	TAGTTGCCCT	GATCTTTTGG	GCTTATACAG	360
TATCTTT	TAAA	ATTACAAGTT	TATTTTGCCT	TGCTCATG	AAATAGTC	AAATTATCCT	420
TGATTG	GCAT	CTTTATGAGT	CTAGCAGCTG	TGGCTAAGGT	TCTCCTGGG	ACTGTGCTAC	480
TTGTAG	CAAT	TGTTATATAT	ATGCTTGCCT	TGCTATTTTT	TGTAGGAATT	GGGATGTGGC	540
ATTTCT	TTAT	CAGTGATATG	TTGGAACCTG	TCTATGAAAT	CATCCATGAA	AAATPGGCT	600

1326

C AAAATAGAA TGAAGCAGTT TTGGCTACAT ACGCTTCTAA GAACCTATAG TTCAGTGTG	660
ATCATATATCA TTGGCAGTTT TCGAATCTTA CTCTCTTACG CTGTCTGGGA TTCACGTC	718

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 718 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

TCGGTACCAA AATTCCTGGAT TTATACTAGC AAAGATCCAA GAGCAAAITA TTAAACAGAT	60
TTAGGTCTAG TTTTCCCTGA ATCATTAAAA GAATTTGAGA GTGAAGATAG TTTTGCAAAAG	120
GAAATTTCTG CAGAAGAAGC AAATAAGATA AATGATGCTG ATGTAATCAT AACTTATGGT	180
GATGATAAAA CTCTTGAAGC TTACAAAAA GATCCTCTTT TAGGTAAAAA AAATGCAATT	240
AAAAATGGTG CCGTTGCTGT AATCCAGAT AATACACCGT TAGCAGCCTC ATGCACTCCA	300
ACACCACCTT CAATAAACTA TACTATTGAA GAATACCTAA ATCTTTTAGG AAATGCATGC	360
AAAAATGCGA AATAAAAAAC AAATAAACCT AGGCATAAAT TTTATAATCT GCCTAGGTCT	420
TCTTATTACA ATATTTTTGT CATTAAAGCT TGGAAACAAA GAAATTAATA TCAGAGATTT	480
TTTAGCAGCT TTTGGAATGG GTAATACAAA TGATGATTTT ATTAATCAA TTATATATAA	540
FAGAAATACCT AGAACTATTT TTGCAATTTT AGCAGGTTCT AGTCTTGCCA TAAGCGGTGT	600
ATTGATGCAA TCAGTTACTA GAAACCCAAAT AGCTGATCCA GGTATCTCG GTATAAACAC	660
AGGAGCAAGT CTTAGTGTAG TAATGGTCC TTCTTTTTCG GGAATTCATC AAGCATAA	718

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GAACATCA TTTTTCACAG ATGAGATTTA CAGCAGAGAG TTTGAAGGCT TTATCAAAAG	60
TTTTTCTTGG CATAACTACT TTCTCTCGTT TCCACTTAAT TTTGTGTCTA CTTTATTATA	120
CCAAGTCCAC sCTTAAGTTA GATAATAAAT CTAACTTAAG GAAGCTAGAA GGATGAGAAT	180
CCAGTGGTTC AAGAGTCCCA AACTTAAGCT GATGGGGACA CCCAGAAATA TTTGCTTTT	240

1327

GAAGGCAAGG CCACGTCCT CTATATTGGG AAGTGAGAGT TGAATGAGAG AACCACTGA	300
TGAAAAGGCT GAGATATTAG TAGATAGAGC GCCAATAACG GTGGCTGTTG TGAGTAAGTG	360
AATATCATCT TGAGGATTTT GAGCACTGAT GATAGCAATG ATGGGAAAGA GGGCTGGAGC	420
TACAACGAT AGGGTGAAC TAAAGAGTGA CATCACTCG GCTATCACAC AAAAGAACAG	480
AGGTAACCAG AATGAGGAA TGCTTGTGT CATGAGGTGC CCTATCAGTG TGACTAAACC	540
TGACTTGACC GCTAGAGACA TTAGTAAGCT CATGCCGAG AGCATGATAA TTGTAGCCCA	600
GGGAACCTTA GCTAAATGG CTCTTGCTT CCTAATTGG AGCCTTAAGG CGAGGCAGAC	660
CATGAGTATT GAGACAAAGC CAATATCAAA TGTTTTTGA TAAGTAGCTA TCCAGCGAT	720
GTTTGGGAAA ATGAGATGCA ACAAGGAAA AAGCCAAACC AUAACCATGC TGCTGATCAT	780
GAGCAAGGTG GTTTGCTTTT GAACCTTGCT GAGGAGTGT GGTGTGCTAA TAGTCAAGGA	840
TGAGTTTGT CTTCCTTAC TATAGTGACT GTAAACAGAT AATAAAAGCA AGACGATGAG	900
TGGGTAGATA ATGCTGACGA TAAAGATATG ATTGCCAAGT GAAAAAGCTT GCTCTTCCCA	960
TCCCATTTGC TTAACAGAGC CTGTAAGAGC AATGCCGTAG CTACTGGTTA TCAATATTAGC	1020
CCCTCTCGAA GCTCCCCAAT TGACGGCTTG AGCTCCAATC AAAGGTGTTT TGTCCGCTTT	1080
TTGACAGAGG GTATTCGCTA GAGGACAGCA AACGGCCATA GTAGTGAATA ATCCAGCACC	1140
TAAAGCAGAC AAAAGGGTTG CCATCAGGTA TAAATCATG TAGAGGGCTT TAGGTGGGT	1200
GGTGTCGCG TAGAGAATGT GTTGAGCCAA AACATCAAGA GTACCGTTAG TTGTTGCAAC	1260
GTTATAAAG AGGAGAGCGC TAAAAATGTT AAAAAAGAT GAGTTTGCC AAAATGAAG	1320
AAGTTCTTG GGGCTTAATC CCATGAGAGT GGTTCGATG AGGTAAGAAA AAGCAATAGC	1380
CAGCAGGCCA ATATTGATT TGTTGGGTA ACCAATTCCA ATGGCTAGAG CAATGG	1436

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1696 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

CCATTTTGGA AAGAAGCTAA GAGTTTGAG GGTGAGATTC CAGAAGAATT TTCAATGTCA	60
GCCCTTGACA TGTCTATGAT TGACCACATT CCAGATATGA TTGAAAAATG GTGTGGACAT	120
CTAAAAATCG AAGGACGTAT GAAGTCTATT CACTACCTAT CAACAGTAAC CAACGCTAC	180

1328

AAGCGGCTG TGGATGCCCTA TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAGAC	240
TTGGTGGACG AGATGTGGAA GGTTCGCCAA CGTGAAGTGG CTACAGGATT TTAATATGGT	300
ACACCATCTG AAAATGAGCA GTTGTTTGGT GCTGCGCCCTA AAATTCCTGA GTACAAGTTT	360
GTGCTGAAG TGGTTCTTTA TGAATGATGG GCACAAACAG CAACAATTGG TCAAGGAAAT	420
GTCAATTACG AAGGGGACCA AGTTGAGTTT TATGGTCCAG GTTTCGGTCA TTTTGAAACC	480
TATATTGAAG ATTTGCATGA TGCCAAAGGC AATAAAATGG ACCGCGCTCC AAATCCAATG	540
GAACTATTGA CTATTAAAGT GCCTCAACCC GTTCAATCAG GAGATATGGT TCGTGCAATTA	600
AAAGAAGGAC TCATCAATCT TTATAAGGAA GATGGAACCA GCGTCACAGT TCGAGCTTAA	660
GAAAGGAAAA GGAATGATA GAGGCACAGG GTTCTTAGT GGATAAGCAA ACAGATGCA	720
TTCAATACCA TAGCAAGCTG GATATTATTG CTTTACAATG CTATGATGTG AAAAAATATT	780
ATGCTTGTTA TCGGTGTCTAT GATTCAATAG AACATCACCC TTTTGAAGCG TATCCCTTAT	840
CTTTGATACA GGATAAGCCT ATTTTATGTG GTGTTTGTCT AAACTACTA ACATAAAGC	900
AATATAAGA AAGCTTAAGT TGCCCCTTTT GTTTTTCTCG CTTTAATCCA GGTTCGCAAA	960
ATCATAAGGA ACGCTATTTT AAATAGCAA TCATCTAGTT TTGAAGTAGG AGAAAATCTA	1020
ATTTCAAGAG AAAATGAAGT AAATCTTCCC ACAATAAAC GCATAATATC AAGATTGTTC	1080
AATACCTGAT ACTATGCGTT TTTAAGATT TAAAGACTTT TTTCCCTTAT CTGGTATTTT	1140
GACTACTGTG TAAAACTGGG TTAATTTTCG ACTGTTTAAT AGTTATTATG CAAAGCTAA	1200
AAGGTAGAA TTGTCAAAAC AATCCGTCTA GAGTATGCGT GATGCCAAC GTGGTGGATG	1260
TTCTCAGTCA TGCCGTGGGA AGTACGACCT TTACGATATG CCATTGGGA AAGAACGTAA	1320
GAGTTTCAGG GGTGAGATT CAGAAGAATT TTCAATGTCA GCCGTTGATA TGTCTATGAT	1380
TGACCATATC TCAGATATGA TTGAAAATGG TGTGGACAGT CTAAAAATCG AAGGACGTAT	1440
GGAGTCTATT CACTATGTAT CAACAGTAAC CACTGCTAC AAGGCGGCTG TGGATGCCCTA	1500
TCTTGAAAGT CCTGAAAAGT TTGAAGCTAT CAAACAGAC TTGGTGGACG AGATGTGGA	1560
GGTTGCCAA CGTGAAGCTG CTACAGGATT TTAATATGGT ACACCATCTG AAAATGAGCA	1620
GTGTTTGGT GCTCGTCGTA AAATCCCTGA GTACAAGTT GTGCGTGAAG TGGTTCTTTA	1680
TGATGATGCG CGGCTA	1696

(2) INFORMATION FOR SEQ ID NO: 298:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

1329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

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CCCAGTTTAT TATGGTTTCT TCGGAATTTA TCTCAAAGAT TGAATTTGCT TGCAATAAGA      60
AAGAAAGTCT TTATAGTCAA AGCAAAATTA AGTATGCGAT TCGTTCGATG TTCGCAGGTG      120
CATTTTAAAC CTTCAGTACT GCTGCAGGTG CAGTTGGGGC TGACTTGATT AATAAAATTTG      180
CACCAGGTAG TGGACGCTTC CTCCTTCCAT TCGTTTTGTC TTGGGGCTTG GCCTACATTG      240
TTTTTTTGAA TGCCGAGTTG GTCACTTCAA ACATGATGTT CTTGACTGCT GGTAGTTTCT      300
TAAAAAAAT CTCTTGAGA AAAACAGCTG AGATTTTACT ATACTGTACC TTGTTCAACC      360
TTATCGGAGC CTTGATAGCA GGGTGGGGCT TTGCTCATTC GGCAGCCTAT CGGAATCTGA      420
CACACGATAG TTTCATCTCA GGTGTTGTTG AGATGAAGTT AGGCCTGCTA AATGAATTTG      480
TCTGTCTTGA GGCATTTTG GCAAAATATT TTGTAAATAT TCGGATTCCTG TCATTTATTT      540
TGGTCAAAGA TGGTGGTGCC AAACCTTGGC TTGTGTTGTC AGCTATTTAC ATGTTTGTAT      600
TCTTAACAAA CGAGCACATT GCGCGGAATC TTGCTTCTTT CGCGATTGTG AAATTCAGTG      660
TTGCTGCGGA TTCAATTTGC AACTTCGGTG TTGGAAATAT GCTTCGCCAC TGGGGTGTGA      720
CTTTCATCGG AAACCTTATC GGAGGAGGCC TCTTGATGGG TCTTCCATAT GCCTTCCTCA      780
ATAAAAACGA AGATACTTAT GTAGATTAAG AAAATGAGCA CGATTGAGTC GTGCTTTTTT      840
CATTTTCAA ATAAGGTAAAT AGCTATTTCT TATATCAAAA TATAGAAAAC TGATATTTGT      900
A=ACTATAAC TCAAGTGCT ACAATATCCT TAATAAAATA ATATGGAGGT CACCTTATGA      960
CTTGTAATTT TAAATnTGAA ACTCTACAAC TACATGCTGG TCAAGTTGTG GCTCCAGCTA      1020
CT                                                                                   1022

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(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

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CCTTAAGTAA TCTCTGATAA TATTTTCTTT ATTAGCATAG GGAATATCG ATATAATGGC      60
TTCATTATGA GTGGCAGGAA TATCCAATAT GGCACTTTT CCAATAGATA ATTTAAAACT      120
CAATTATAAA GTTCCTTTAG GTGAAATGTC TATTTTCTTT GATTTTAATG CTAAATTTAGA      180

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1330

AATAGATTCT CTCGCATTAG TTACATAACC AGATATAGGC ATATCTGATA TAGATACCCA	240
AGGTATTTCA GTCCCCAAA AAGTAGCTTC ACTGCGTGGG GGAGTTTTTC CTATCTCTGAA	300
GTTAACTAGG CTAGCAAAAT TAATATATCT CCATGCTTCT GGGATTTTCA ATATAGGATA	360
AGAGGTTGTT TCGTCTTTGT TCCCATATA AGAGTTATCA TCTCCTTGGG AAACANTAGA	420
AATGTCCAAA TCTTCTTTT TAATCTTGCC TTCCTCAAAG AGTTTTGTT TTTCTGCTCG	480
TATTTTTCA AGTAAACTT CGACTGATTC ATCATTTGGG TCTGTTCAA CTAAATTTCC	540
TTGCATAGCA TATTGAAGAA TAGATTTTTT TAGTTTATCT GGAAATCTTT TATCTAGCTG	600
TTCAGTCTTA TTATAACTTT CAGCATATTC ATCTACTTTT TCTAAAGCTG ATTCGATTGC	660
TTC	663

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 881 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

CGTCGCTGAA CATGTCAACA GCAAAATAAA CTAACAAAC TAAATATG TGATACTTCA	60
CATAATTTTC TTGAAAAAT ATTATCAGAA GAAAGTTGAG AAAAATGGCA GAAAAACAT	120
ATCCTATGAC CCTTGAGGAA AAGGAAAAAC TTGAAAAAGA ATTAGAGAA TTGAATTTGG	180
TTGCTCGACC AGAAGTGGA GAACOCATTA AGATTGCCG TTCATACGGT GACCTTTCAG	240
AAAACAGTGA GTACGAAGCA GCTAAGGATG AACAGCCTT TGTGCAAGGA CAAATCTCTA	300
GCTTAGAAAC AAAATCCGC FATGCTGAAA TCGTCAATAG CGACGCAGTT GCCCAGGACG	360
AAGTAGCGAT TGGTAAACA GTCACCATCC AAGAAATVG TGAGGACGAA GAAGAAGTTT	420
ATATTATCGT AGGTTACGCT GGTGAGATG CTTTGTAGG TAAGGTTTCA ANTGAAGCC	480
CAATTGGGCA GCCTTGATT GGCAAGAAAA CAGGTGATAC AGCAACCATT GAAACGCTG	540
TTGGTAGTCA TGATGTAAAA ATCTTGAAAG TTGAAAAAC AGCCTAAAA CAGAAAAAGG	600
AGTGGGGAGG GATGTGCTT CACTCACTCC TTTTCCATT TTGCTACTCT TCGAAAAATCT	660
CTTCAAAACA CTTACAGCTC GCCTTGCGT ATGTATGGTT ACTGACTTTG TCAGTTTCAT	720
CTACACCTC AAAACAGGT TTTGAGCTAA CTGCTCAGT TTCATCTACA ACCTCAAAAC	780
TATGTTTTGA GCTGACTTCG TCAGTTTCAT CTACACCTC AAAACCATGT TTTGAGCCGA	840
CTTCGTCAGT TTCATCTACA ACCTCAAAAC TATGTTTTGA G	881

1331

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 949 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

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CCTTTTAA TACAAGTTAT TTTGATTAA CCGCTTGTC TTGAGCTGTC TGCAAGCTG      60
TGGCAATCGT ATCTGCATAC AATTTTGCTC CTGCTTGAT AGTGCTACTC TCACATCCCA      120
AATGAACCTG GTCTGTTCCA GCCCAAATTT CTGGATGCTC TTTCGCAACT TGATTCCAAT      180
CTGCTATCGT AATGTAAGGT GTCTTCTCTG CCAATTCCTC CATATAGCA GCAGCCTTCT      240
CAACGATGCG ATAGGTCTCT TTTGTCTTAT CTCCTCATA AGGAGTCACC AAAATCATAT      300
GGTGTCCTT AGGAAGATT TCCACGATAC TGTCCAGTTC ATCTTGTA TTCTCAGGAT      360
TATTACCC AGTCGCAATG ACCACGCTCT TAGGTAAGAA TTTATTCCTG CTATTATTTA      420
GCATGATTC ATTTGCGGTG TTGGTTGTTA CGCTGACCTG CGCGTTAATC TGTGCTCCAG      480
GAAGAGCTGT CTGTAGTGT GTATTGCCC TTAAAGCCAC TGAGTCACCA ATTAAACATAG      540
TGCCATCAGC AATTCCCAAA CTGTTTGCTT CTGCCCGTTC TGCCATCACC TTGGTCTGGC      600
CAATATTGTG TGCAGCTTGC TTCAAGCCAT TGACAGTCAA GTCTGTCTCA AACGCTCCCA      660
CTTGCTGTGC CAACAAGTTC ACCGTGCGA CAATGATGTT CAAGATTCCT GTACCTGCTG      720
CAAGAATTGC GTGAATATAA GGCAGGGGAC GAAGGGTTTG GACCAATAGT GTGTCTGTGC      780
CTGCAATCCA AGGTTCCAT ACATAAAATG ACAGACTGGC AAAGCCATAA GAACAAATCA      840
GAGTCAGTAA TACAGCAAGA AGATTGATG TCAACTGTGA GAAATGATA TAGAAGGCC      900
AATGGAAAG ATAAACCGCA TAGCTAGTAT CCGCTAAAAA GCTGATAAT      949

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(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

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AAGATATATT TTTACACAG AAGTATGCAA AAGTAAAGAG TGCAAAAAAT GCAATTAAG      60

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1332

CGAAATATA AGCCGTGTAC AGGCGACCAA ACCAAGTAC ACGGCTAAGG AAAATAACA	120
AAACTCAAGC AAAGGCAAGC CGCCTGGTTC TGTTAGGTAT TTAGCAAGGG GACAAACCCC	180
TTTGTAATA ATCTCCTCTT ATTTTATCAA AATTAGAGGA AAATGACAAC TTAATTATATA	240
AAAAGGAAAA ATGGAGGATA TAAATGGAAA TTCTGTCTTA AGAAATACAG TTACAGGGCT	300
TACAACTTCT TAAACAGACT CTTGAAACTT TGGTTGAGCT AGAAAAACAA CGATCTAGTA	360
AGTTAGATTT AATTCTCTGT AAAGAAATTA TGGATCTGCT AGGTATAAGT GCTACAACCC	420
TTGATAACTG GGAGGATCTT GGTCTTAAAC GATATCAGAC TCCGATGGAT GGAGCTAAGA	480
AAGTATTCTA TCGTCCGTCA GATGTGTATT TATTTTTCAG AATAAAATAG GAGTTATGAA	540
ATGAAAATCG TTAAGTTTCAA ACCAACTAAA CAAATAGACG ATGGGTTTTA ACTGCCAGGT	600
ATGACATTC TATTTGTCTC AG	622

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1929 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

CGCTAACTTG CAAACAAAG AAGAAGCGAA ACTCCACAAA TCCTTTACGC AGAAACTCAA	60
TCTCATCTAC TTACCTTGCT GACTTGGTAG AGTATGTTGC AGACAAAGAC TTCTCACTAA	120
ACGTAAATTC TAAATCAGGT ACAACAACAG AACCAGCGAT TGCTTTCCGT GTCTTTAAAG	180
AACCTCTGGT TAAGAAATAC GGTCAAGAAG AAGCTAACAA ACCTATCTAT GCAACAACAG	240
ACCGCCAAAA GGCTGCTGTT AAGGTTGAAG CAGACGCTAA CGGTTGGGGA ACATTTGTTG	300
TTCCAGATGA TATCGGTGGA CGCTTCTCAG TATTGACAGC CGTTGGPTTG CTITCAATCG	360
CAGCATCAGG AGCTGACATA AAAGCTCTTA TGGAAAGTGC GAATGCAGCT CGCAAGACT	420
ACACTTCAGA CAAATCTCTT GAAACGAAG CTTACCAATA CGCAGCTGTT CGTAACATCC	480
TTTATCGTAA AGGCTATGCA ACTGAGATCT TGGTAAACTA TGAGCCATCA CTTCAATACT	540
TCTCAGAAATG GTGGCTGGTG AATCAGAAAG AAAGACCAA AAAGGTATCT	600
ACCCAATTC AGCCAATTC TCAACTGACT TGCACACT TGTCATATTT ATCCAAGAAG	660
GAACTCGTAT CATGTTTGAA ACAGTTGTCC GTGTTGACAA ACCTCGTAAA AACGTGCTTA	720
TTCTACTTTT GGAAGAAGAC CTTGACGGAC TTGTTTACCT TCAAGGAAAA GACGTTGACT	780
TTGTAAACAA AAAGCAACT GACGGTGTTC TTCTTGCCCA CACAGATGCT GATGTACCAA	840

1333

ACATGTATGT GACTCTCCA GAGCAAGAGC GTTTCACCTCT TGGTTACACT ATCTACTTCT	900
TGGAATTGGC AATTGCCCTT TCAGGTACTT TGAATGCTAT CACCCCATTT GACCAACCAG	960
GTGTTGAAGC TTATAAACGT AACATGTTTG CCTTCTTTGG AAAACCAGGA TTGGAAGAAAT	1020
TGAGCAAGA ACITTAACGA CGTCTATAAT AGAAGAAAAG AGTGGTTTGC CCACCTCTTT	1080
TACTCTCTTT ATCCATAGAA ATTGGACTCA GCCAAGACTT GTGATATAAT ATAGAAAGCA	1140
AAAAGGCAGA CGCTAGATA ATAGAGGAAA CTATGTCAAA AGATATCCGC GTACGTTACG	1200
CACCAAGTCC AACGGACTA CTACACATCG GAAATGCTCG TACAGCATTG TTTAATTACT	1260
TGTATGGCGC CCATCATGGT GGAACATTTC TCATCGGTAT CGAAGTACT GACCGTAAAC	1320
GCCATGTCGA GGATGGTGAA CGTTCACAAC TTGAAAACCT TCGCTGGTTA GGCATGGATT	1380
GGGATGAAAG TCCAGAATCA CATGAGAATT ATCGCGAGTC TGAGCGTTTG GACTTGTATC	1440
AAAAATATAT TGACCAACTA TTAGCTGAAG GAAAGGCTTA TAAATCTTAC GTTACAGAG	1500
AAGAGTTGGC AGCTGAACGC GAACGCCAAG AAGTAGCTGG CGAACACCA CGCTACATCA	1560
ATGAATACCT TGGTATGAGT GAAGAAGAAA AAGCAGCTTA CATCGCAGAA CGTGAAGCAG	1620
CAGGGATCAT CCCAACCTGT CGTTTGGCTG TCAATGAGTC AGGTATCTAC AAGTGGCATG	1680
ATATGGTCAA AGCGGATATC GAATTTGAAG GTGGCAATAT CGGTGGTGAC TGGTTATCC	1740
AAAAGAAAGA CGGTTACCCA ACTTACAAC TTAGCGTTGT TATCGATGAC CACGATATGC	1800
AAATCTCTCA TGTATCCGT GGAGATGACC ATATTGCTAA TACACCAAAA CAGCTTATGG	1860
TCTATGAAGC TCTTGGTTGG GAAGCTCCAG AGTTCCGTCA CATGACCTTG ATTATCCACT	1920
CTGAAACTG	1929

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AAATTGAAGA AAAAGGAGAC ACATCATGTC TAAAAAGTA TTATTTATCG TCGGATCACT	60
AGTCAAGGT TCTTTCAACC ACCAAATGGC GCTCGAAGCT GAGAAAGCAC TTGCTGGTAA	120
AGCGGAAGTT AGCTACCTTG ATTATTACGC CTTTCTCTC TTCAGCCAAG ATTGGAAGT	180
TCCAACACAT CCAGCTGTAG CTGCTGCTCG TGAAGCAGTT CTCGTTGCGG ATGCTATCTG	240

1334

GATTTTCTCT	CCAGTCTACA	ACTTCTCTAT	CCCTGGTACA	GTGAAAACT	TGCTTGACTG	300
GCTATCTCGT	GCCCTTGACT	TGCTTGATAC	AGTGGCGTT	TCTGCCCTTC	AAGACAAAGT	360
TGTCACAGTA	TCATCTGTAG	CCAATGCAGG	GCACGATCAA	CTTTTGCTTA	TCTACAAAGA	420
CTCTCTGCCA	TTTATCCGTA	CACAAGGCOT	TGGTGATTTC	ACTGCTGCAC	GTGTPAATGA	480
CTCTGCTCGG	GCACACGGAA	AATTGGTTCT	TGAAGAAACA	GTCTTAACCT	CACCTGAAAA	540
ACAAGCTCAA	GACTTGGTCG	AAGCTATCAA	GTAACATAACA	CTCAATAAAA	ATCAAAAAAGC	600
AACTTAAGAA	GCTATCCGCA	AGCTACTCBA	GCACCTGCTTT	GAGGTTGTAG	ATAGAACTGA	660
CGAGTGTnnA	ACATATATAC	GCTAAGGCGA	CACCTGACGTG	GCTTGAAn		708

(2) INFORMATION FOR SEQ ID No: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID No: 305:

CTTCTTTTCT	TGGAAATAGG	TGTATAATAC	GTTTATTAAA	TTTTTGAGGA	GTGTCTATG	60
AAGAAAAAGT	TTATCCATCA	ACAAGAGAA	ATTTCCCTTG	TCAAAAACAC	TTTACCCAG	120
TATTGTAAGG	ATAAGCTAGA	AGTTGTCCAA	GTTCAGGTC	CTATCTTGAG	TAAGSTOGGT	180
GACGGAATGC	AGGACAACT	GTCTGGTGTG	GAAAAATCCAG	TATCGGTCAA	GGTCTCCAA	240
ATCCCTGATG	CTACTTATGA	AGTGGTGAC	TCACCTGCTA	AATGGAACG	CCACACCTTG	300
GCTCTTTTG	GCTTGGTGA	AGGAGAGGGT	CTCTTTGTCC	ACATGAAGC	CCTTCGTCCA	360
GATGAGGATT	CCTTGATGC	AACCCACTCT	GTTTATGTTG	ACCAGTGGGA	CTGGGAGAG	420
GTTATCCCAA	ATGGTAAGCG	TAACATCGTT	TATCTAAAAG	AAACAGTTGA	GAAGATTAT	480
AAGGCTATTC	GCTTGACTGA	GCTAGCTGTT	GAAGCCCGCT	ATGACATCGA	GTCTATCTTG	540
CCAAAAAATA	TTACCTTTAT	CCATACAGAA	GAATTGGTAG	AACGCTACCC	AGACTTGACA	600
CCGAAGAAC	GTGAAAATGC	GATTGTGAAA	GAATTGGAG	CCGTCTTTTT	GATTGGTATC	660
GCTGGCAGAT	TGCACAGATG	TAAACCCAC	GATGGACGTG	CACCAGACTA	TGATGACTGG	720
ACAAAGCAGT	CTGAGAAATG	CTACAAGGCT	CTAAATGCTG	ATATTCTCTG	CTGGAATGAG	781

(2) INFORMATION FOR SEQ ID No: 306:

(i) SEQUENCE CHARACTERISTICS:

1335

(A) LENGTH: 846 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

CCGCGATCTT GTAGGGTTTT AACGGGCACG ATTTTCATAT CCGTCTTGAT TGITTTAGCC	60
GCTTCTAGGG CTGTTTGTA GTTGTTTTC GGTCCGGAT GCGCCTTTTG TTCTTCTTCG	120
CTAACAGGGT TATCAGGAGC AAGAAAAATA GCAGCACCTG CCTAGCCGA AGCTACAACC	180
TTCTTATCAA TACCTCCAAT GTCTCCACA TTACCATGCG GGTCAATGGT ACCTGTACCG	240
GCAACAATAC GACCATTACG AAGATCTGGG TGAGCTATTT GAGTATAGAT AGCTAGACTA	300
AACATGAGAC CAGCACTTGG ACCGCCAATA CCAGCTGTTG AAAAGCTAAT TGGGACATTG	360
CTGATTACCT CTGTACGGTC AATCAAGCG ATTCAAATTC CATTTTGGCC ATTTTCCAAG	420
GTGATGATTT TTCTTCTGC AGACTTGGTT TGCCCATCCT CTTTCATAGT GACCTTGAGC	480
GAATCCCCTA ATTTTGTAGA ACTGACGTAA TCAATCAAGT CTTTGGAAC ATCAAAGGTC	540
TGATCATTGA CTGCTGTGAC TGTATCAGAG ATATTGAGAA TCCCTTTAAA GGTGGAATTA	600
TCGGTCACAT TCAAAACATA AACTCCAAAG TACTTGAGTT CGATATCCTT ACCAGCTGTT	660
TTTAGTCCCT GATACTTGGC CATATTTTGC GATGTTTGCA TGAGAAATPG ATTGATTGCG	720
ATAAATTCAA CATCGGAAGA ACCACCTGTA GTCTCTGAG CACTACGAAT ATCTGTAAAA	780
GGTGTCACCC AAGCATAAAT CATATGAGCT AAAGTGGCAT GTTGAACACC AACCGTAACC	840
AATTGT	846

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GCGATCTGCT TGGGCTTTTC CTATTACCTT ATCTAATAAA TAGGTACGCA GACTCATAAC	60
CATATAAAGT CCACCCCCCA TGGCACGAC AAGAGCTACA TAAAAGAAGC TCCACAAAAG	120
TCCACTTGGT TGGAGAAAA ATCTTAACAG CCACGGATG GTTCCTATTA ACAGAAAAT	180
GACTAGGGTC AGCAAACTGA TAAAAATGGT TCGCTTCAAA ATCACTTGC GCTTGACACC	240

1336

AGTTACTTTA CAAATATCCC GATACATCAA GACGTTAGGA ATGATGAGAG CAATGGTTGT	300
TGAAATCAAA GGACCAATAAC TGTGGAAGAG GCGATGGTA GGTAGTTGCA AGACTAGCTT	360
GGCAATAGAA CCATAGATAA AATAGAGAAC GGCCTTGCGG TTCCGGAACA TGGCCTGAAG	420
CATTTGGAGAC AAGACCATGT ACAAGCCTAA AATAATAGAC TGCAAAACTG CAAAGACAAA	480
TAAGCCGAGA GCCAACTAT CTGGCTTACC ATAGAAGACC GTATAAGAG GTTCTCCTAC	540
CATAACCACT CCAACCGTTG CTGGTAGCAA GAACAATAAG AGTAGGGTGA GACTGTCTCG	600
AACGAGACGA GAAGCTGCTT TCAAGTCCCC CTGACATAG TTTTCCGTCA AAAGTGGCAA	660
ACCAACACTC CCAATCGAAA CCCCTACAGA AATCAAAATC ATCGTGATTT TATTAGGATT	720
GCCTGAGAAA TAAGAAACA TGACAACCAA GTCTCATTTG CTGTAGTTGG TAAACCAGCT	780
CATACTATTG ATAAAGGTCA GCTGAGTCCA AATCTGGAAG AGCTGGATG	829

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 464 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CGAACATCTT GCTGGCTGAT TCGTCTGCC CCATCGCAGC CCCGAACACA TTGCGACCCA	60
TGGCAAGCGG GCTCAATCCG CACATGGGAT CCGTGCCAAA GCCCGCGGTG TGCATCATTT	120
GCTCATCTAG TAAAGTATGA GGTTCGCCTT CGCTGTCGAT AAACCGATAT TCAATCGCAC	180
CACCTGCTGT TCTCCGCGGA GGGGAAACCG ACTGCGGTAG GATGAATCC AGAGAAGAGA	240
GATCAGCACC TACCAGGTGC GGCTCGTTGA AGCTGTTGCC GCTTACGAGC AGGCTCGCCA	300
CCACGCATTC CCAGAACTCA ACGGGGGTTT GATCGGGGTT CGGTTGCTGA CTAATAACTC	360
GGTGACCGGG ATGCGAAGTG GCCACTCTTG GCACACCGTT CTGTCTCTCG TAGAGAGCAA	420
TTGGGAGGGT GGCCAGCGTT TCGGCGATGA GGCGACGCA GGC	464

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 982 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

1337

CCGCTCTATAA TGGTAATAGA TTTTATTGAG AGGTTTATTAT GTCAATTCTA TCAAAAAATG 60
 GAGCAGGTAT CTGGCCCTGC CTTCTCATTT CCATCCCTATC TTGGTACTTA GGAGGATPCT 120
 TCCCCTGTGT TGGCGCGCCC GTTTTTCGCA TTTTCATAGG CATGCTCCTA CATCCCTTTC 180
 TCTCGTCTTA TAAACAACTG GATGCTGGTT TGACCTTTAG TTCCAAGAAG TTGCTCCAAT 240
 ATGCCGTTGT CTGCTTGGT TTTGGTCTCA ATATCTCGCA GGTCTTCGCA GTTGCCCAAT 300
 CTTCACTCCC TGTCATCCTG TCCACTATCT CAATAGCTCT GATTATATGCC TACCTCTTCC 360
 AGCGTTTCTT TGCCCTGGAT ACAAACCTGG CTACCTTGGT TGGAGTAGGT TCTTCTATCT 420
 GTGGGGGTTC TGCCATTGCA CGACAGGCC CGTTATTGAT GCTAAGGAAA AGGAAGTAGC 480
 CCAAGCCATT TCCGTTATCT TTTTCTTCAA TGCTTGGCT GCGCTCATCT TTCCAACCTT 540
 CGGCACCTGG CTTCATCTAT CCAATGAAGG CTTGGCCCTC TTTCGAGGGA CTGCGGTCAA 600
 CGACACTTCC TCTGTAACGG CTGCCGCCAG CGCTTGGGAC AGTCTTTACC AAGCAATAC 660
 CTTGAGTCTT GCAACCATTT TAAACTCAC AGTACTTTG GCATTATCC CTATCACGCT 720
 CTTTCTATCC TACTGGCAAA GTGCCCAACA AGAAACAAG CAAAGCCTGC AACTGAAAAA 780
 AGTCTTCCCA CTTTTTATCC TTFACTTTAT CCTTGCCTCT CTCTCTACTA CACTACTCAC 840
 CTCTCTAGAT GGTGCCAGTA GTTCTTTTAC TCCTCTCAAA GAATCTCTA AATTCCTTAT 900
 TGTATGTGAC ATGAGTGCTA TCGGTCTCAA AACCAATCTG GTGCTATGG TCAAAATCCAG 960
 TGGAAAAATC ATTATCATG GA 982

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1939 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

CTAGCTGCCA ATATGATTGG GTGCGAGAAG CGCGTGATTA TCTTTAATCT TGCGTTGGTT 60
 CCTGTGGTCA TGTTTAACCC AGTGCTTCTG TCCTTTGAAG GATCCTATGA GGCAGAAGAA 120
 GGCCTTTTGT CCTTGGTAGG TGTGAGATCA ACTAAGCGTT ATGAAACCAT AAGGCTTGGC 180
 TATCTGTGACA GCAATGTGCA GGAACAGACC ATTACCTTTA CAGGCTTCCC AGCTCAGATT 240
 TGCCAGCATG AGCTGGATCA CTGGAAGGA CGAATCATTT AGGAGGAAAG CAAATGAATC 300
 GAATAGTCTT TGAACCTATT TTTATCGCAA CGACCTGGTA TATCTTTTFA CCGCCCTTTA 360

1338

ACCTGACCAG CTGGGAATTT CTCTCTCTCC TCTGTGGGCA TTTGTAGTGT GTGGCAATAT	420
TATTTGGCTT TGGCAAGGG ATAAACCTTG TCAAAACGGT TCAATGTGGC CACGGTAAGG	480
CGGAAGCTGC CTTAAATCTT GAGGTTTCA AAATCAATCG GTTAGGGAAA ATTCTGTTAG	540
CTTCGATTGG AGGAATCTTT CTCTTGGCAG CTTTGGTTCT CTTGGTAACT TCCAGCATGT	600
TTCAAGGCTAA AAATTAATGCC AATGTAGTCA CGGTTACGGA AAAGACTTT ACTGAATTC	660
CTAAGAGTGA CACCGTAAG GTTCTATCC TAGATAGAAG CGTAGCGCA GATACCTATA	720
ACCGCTACTT GGTTTCCCTA ACCGATAAGG TGTGCAATA CGTAGCGCA GATACCTATA	780
CCCAATGAC AATTGATGG AAACCTTATC GGGTCACACC ACTAGAATAT GCAGACCTTA	840
TCAATGGTGT TAACAATCAA GCCAAGGGAA TCGGTGAGTA TATTAAGGTG GACATGGTAA	900
CTGGAAATGC GGATTTGGTG GACTTGAAGA CACCAATCAA GTATTACAGC TCGGAGTATT	960
TTAACCGTGA TGTCAAACGT CACCTGGCT TGAAGTACCC GACCAAAATC TTTAAAACTC	1020
CATCTTTTGA GGTGACGAT GAGGGCAAT CTCTCTATGT AGCAACGGTT TACCAAAAGC	1080
AATTTGGACT TGCTGTTCTT CGTCTGCTT CAGTCAITAT CTTGGATGCT ACAAAATGGAG	1140
AAACCAAGGA ATACAGCTTA TCAGATGTTT CAGAATCGGT GGACAGGATC TATCCAGCAG	1200
AGGAACCAT TGAGCAATC AACTACAACG GCAAGTACAA GGACGGTTT TTGAATGCCA	1260
TGATTTCCAA GAAAAACGTG ACCCAGACTA CCAATGGCTA TAATTACTTG TCTATCGGTA	1320
ATGACATCTA TCTCTACACA GGTGTGACGT CGGCTAATCG GGATGAGAGT AATCTTGGTT	1380
TCATCCTTGA AAATATCCGA ACAGGAGAAA TCACTAAGTA TAGCTTGGCT TCTGCGCAG	1440
AAGAATCAGC CGGTGAATCA GCAGAAGGTG CTGTTACGGA GAAATCCTAC AAAGCAACCT	1500
TCCCAATCCT CATCAACCTC AATGACAAGC CTCTCTACAT CATGGGCTTG AAGGACAATG	1560
CTGGCTTGGT CAAAGAGTAC GCCCTGGTAG ACGCACTCGA GTACCAAAAT GTTATCGTTG	1620
CTACTACAGT GGAAGAGATG CTCAGCAAGT ATGCCAATAA AAAGACCTT GAAATGACA	1680
ATGCAACGAC AGAAAGCATC AATGGAATAG TAGCAGACCT CAATCAGCT GTTATCAAGG	1740
GAGACACTGT CTACTTCTTT AAAGTTGATG GCAACATCTA CAAGGTCAAG GCTTCAGTAT	1800
CCGATGACCT TCCTTACCTT GAAATGGTA AAACCTTCGA AGGTCAAGTA GGAAGAGACA	1860
ATTATCTCAA GACCTTTAAG CTACGGTAAA AATAGGTTTT TTTCAAGAA GATATGTTAT	1920
AATAAGGTAA ATTAAGCCG	1939

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 907 base pairs
 (B) TYPE: nucleic acid

1339

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

CCTGCTAATA GAGAGAAAGA CTAGGAGTAG AAGTAAGCCA ATTAATAAT GAGAAAGTTT	60
CATACCCCGT CCTTTCATGT AGATTGGTA TCGAAGATA TCTGCCGATA TAAATGTAAC	120
ATTATTTTTC TAATCTGTCA ATAAATTTTC TGACAACTTA ATAAATACAA CAAGGAGAGA	180
GCAACAAGAC TTCTCCTTT GTATCCTAT TCTAAAAGT TTTTACCTTA ATCTGATAAA	240
ATAATATCTT CGAGGGAGTA GCTAGCCGTC CAATCAAGAT ATTGTTAGC TTTTGAAGCA	300
TCTGCTAGGA CACTGGCTGG GTCACTAGCA CGTCGAGCAA CAATCTCGTG TGGGATTTT	360
TAATTTAGTA ATTCTTCAGC AGTTTTAAG ATTTCTTTGA TAGTATAGCC TTTTTAGTT	420
CCTAAGTTAA AGATTGAGA AGAACTGCT TCTTGAAATA GGTAGTTCAT TCTTTAACA	480
TGAGCTTATG CAAGGTCCAA GACATAAATG TAATCTCGAA TACATGAACC GTACAGTGA	540
TGCTAGTCAT CTCCAAATAT TTTTAAGCTA TCATTTTGC CCAATGCGGT CTGTTGATA	600
TTTGGAATGA TGTGAGTTGG ATTTTTCACA CGCAGACCGT TTGAAGCATC CATTTACGCC	660
CCAGCAACAT TAAAGTAAAG GAAATAACA TATTTCCAGT CGTAGCGATT GGCATCCAG	720
TAAATCAATC GTTCGCCAT CAGTTTGTG TCTGCATAAG GGTGACAGG GTCGAGCAGG	780
GTATCTTCAG TCACCGGCTT GTCAATACAG TTATTTCCAT AGAGAGAAGC AGTCGAAGAG	840
AACATGATTT TTGAAATGCC AACTTCAGAT AAGACTTGA GAACTTGGT CATACCAGCA	900
ACGTTGG	907

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2170 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CCACATAAAG GTAATATCT TTGTACTAT CTGGGCATC CAAGAAAAGC AATTGGGCAA	60
TAAACAGATT AGCCATATTG TCTTCAACCG GACCTGTCAG CATAATGATG CGGTCTTTGA	120
GAAGACGTGA GTAATATCG TAAGAACGTT CTCCACGGCT TGTTTGTCA ATAACACAG	180
GAATCATCA TTTCTCCTTT TGAGTTTAA TTTTGTGGT CAAATGACTG AAGATAAGAC	240

1340

TATTATAATA TCTTGCTCAA AAAAGGTCAA ATTTTGTCTC TGCTTTCATT AGACAGAAAC	300
AAAAACCCAA CCTCCTTTGG TGACTGGAAA TACTTTTCCA AGTCATTCTT CTTTTCGATC	360
TTATTTTGTA CGGAACAAGC GGTCTCCAGC ATCTCCAAGA CCTGGAACGA TATAACCGTG	420
TTGGTTCAAA CGTTATCCAA AGGCTGCTGT AAGATTTCT ACATCTGGAT GAGCTTCTTG	480
AAGGCGTTTT ACACCTCTG GAGCAGATAC AAGGCACACA AATTTGATAT TTGATGGGCC	540
ACGTTTTTTA AGAGAATCAA CAGCCAAGAT TGCTGAGCCA CCGTTGGCCA ACATTGGGTC	600
TACTACAAAA ATTGACGTT GGTCAATGTC CTCAGCCAAT TTCAACCAAGT ATTCAACTGG	660
TTGAAGTGT TCTTCATCAC GGTACATACC GATGTGGCCA ACTTTAGCAG CTGGAACCAA	720
GTTCAGAGA CCATCAACCA TCCCGATACC TGCACCCAAG ATTGGGACGA TGGCCAATT	780
CTTACCTGCC AATTGTTTT GAACGTGTTT TGTAAITGTT GTTTCGATTT CCACATCTTC	840
TAGTGGUAGA TCACGAAGTA CTTCATACCC CATCAACATT GCAATTCAT CTACTAGCTC	900
ACGAAAGCT TTTGTAGAAG TATCTGTACG ACSCAAGATT GACAATTTGT GTTGAATCAG	960
TGGTGATTA ATAACTTCAA TTTTTCOCAT TTTTGGAAAT CCTCTTTTCA ATTTATTCTT	1020
CTTATTATAC CAAAAACCG TTTAAAAATC TTCTTAAACC ATTTATTTTT GATAATTTTT	1080
ACATTTAGATC AGCCTCTTTA AGAGCTGTCT GTACTGTCTC AAGTGTGAAA TGGGTCAATT	1140
CTGTCCCTTT TCTTGATAA AGGTATTGGG CGTAGTGTC CATTCGGTAC TGGTTGATAT	1200
AAACCAACGC CTTCGACGGC ACCTGAAGCA ATTTGTTTGT ACAGTTGAGA CAAGGAAAT	1260
GGGTACATA GGCCTGAAAG CCTTTGGGAA CACCACGCTC AGCACCTTGA AGGATAGCAT	1320
TGACCTCAGC GTGAAGGGTG CGAACGCAGT GGCCTTCAAT GACCAACAT TCGTGATCAA	1380
TACAATGCTC AGTCCTTGAC ACOGAACCAT TGTAAACAGT GGAATAAACC TTATTATCTT	1440
TTACCGAAT CGCGCCCACT TTAGCACGTT TACAAGTGA ACAGATTGCA ATTAGTAGAG	1500
CTTGGGCTGC AAAATACTCA TCCAGGCCA GTCTTTTTTC AGTCATCTCT TTTCTCCTTT	1560
TTCTCTATT TTAAAAAAT GGTAAACCTA AATCTGCAAT CPTTTCAGCT GTTACCTTCA	1620
TGCCATCCTT GATCCATTTT AGAAGGACAG AGACGATGGC TGAGCTCCAG AAGGAATGAA	1680
GATAAGAGCT GACACCTTTT GATTTCCCAT GGTATTTTTC TAGAAATTCG TGCATGGCTT	1740
GGACAAAGAT TTTTTCAGTA TGGTAATCCA AGGCCAATTG AATTACTCTA GCTTCTTTTC	1800
TGGCTCCCG GAAAGGTGA ACCCAAAACA AATAAAGGTC TGTCCTTAAA TCGTATGAT	1860
GCAGCTGTTC CATATATTTG TGGACAGTTC GTTTAAAGAC GCTCTCTAAA ATTTCTCTCT	1920
TGGAGTCATA ATTGCGATAA AAGGCCGCAC GCGAAACACC TGCACTTTTG ACCAATTCAG	1980
AAATACTAAT CTTGGTCAGT TCCTTTTTTT CCAAGAGTTG CAAGAGGGCT GTTTCAATGG	2040

1341

CTTCTCTGGT TAAATAAATG GATTCTTGGT TTGATTTTCT GAGATTTTCA AGAGACTTTT	2100
CAGAGATTCT ACGTTCAGAC ATAACATTTT CTTTCTACTT GTACACAACAG ACGGATGATG	2160
CTTTTGTGTTTC	2170

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

ATCTGCACGA ATCAGGGCTT TCTAAGTGAC TATTTCCACC GAAATATTAT TTATATCAGG	60
AGGACATTCA TATGTCAGGT TATACAGGAC CATCTTGGAA ACAAGCTCGT CGTCTTGGCC	120
TTTCACTTAC AGGTACAGGT AAAGAAATTGG CACGTGTGTA CTACGTACCA GGACAACAGC	180
GACCAACAA CCGTCTAAA TTGTCAAGAT ACGTTTGCA ATTGGCTGAA AAACAAAAC	240
TTCTGTTTAC TTACGGTGTG GGTGAAAAAC AATTCGTGA CTGTGTCGTA CAAGCTACAA	300
AAATCAAAGG CGGAATCCTA GGTTCAACT TTATGCTTCT TTGGGAACGT CGTTTGGATA	360
ACGTTGTTTA CCGTCTGGT CTCGGGACTA CTGTCGTCA AGTCGTCAA TTCGTAACC	420
ACGGTCACAT CCTTGTGAC GGGAAACGG TTGATATCC ATCATCCGC GTAACTCCAG	480
GTCAAGTGAT CTCAGTTCT GAAATATCAT TGAAGTTC AGCAATCCTT GAAGCAGTA	539

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCGGTTTTC TCCTTCTCA CGGCTACGAC GTGATGTATC TCTGATGATA TCCACTGTTT	60
CTGTAGCAGG CGTAGGTGTT TCTGGACCTG CTTGTTCTGC TTTTCTCTCT GCGTCTGAT	120
AGGAAACAGC TACCCTTGT GGGGTTTCT TGTATTCTCT TTCAAGTTTC TTAGGTCATA	180
CAGGACCTGG ACCTGCTCTT GATCCACTTT CTTCGCTGG AGAAGAAGGT ACATCTTGAC	240
TTGGATGACT TGGAACCA CGAGTTTCTC TTGAATCTC ATCTGCTGGA GAAGCTGGTA	300

1342

CACCTTGACT TGGGTGAGTA GGCACGGTAG GAGCTTTCT CATATCTCC TCTACCGTTG	360
ACAAGGAATC AGCCATGAGT TCTTCAGTTG AAGGTTCAAT TGCAGGAGTG CGAACTACTG	420
CCTCATCTTC TTTCAGAACT TCATCATAGC CTTTACTTTT TTCTAAATCT CTCGAAATCT	480
CCTCTTTAAA GCGTAATTC TCTTCTGCTC TTTGACTTTTC ACTCAAAAGT TTTTCTCTCT	540
TGTTGAGGAT CATATAATTT AGAGCTGAGA ACTCCAAAAA AAGCAATCTA TGATACTTTT	600
CCTAACGGAT TTTGTCTATT CCCAGACCAT ATCATACCAT GTTTCCTCCG: CAAAGGTTGA	660
CTGGGAA	667

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA GGTATTTTAT CGGATGAAGT TGTACTAGT TCTTCACCGA TGGCTACAAA	60
AGAGTCTTCT AATGCAATTA CTAATGATTT AGATAATTCA CCAACTGTTA ATCAGANTCG	120
TTCTGCTGAA ATGATTGCCT CTAATTCAAC CACTAATGGT TTAGATAAAT CGTTAAGTGT	180
TAAATAGTATC AGCTCTAATG GTAATATTCT TTTCCAAATCA CAATTAGACA ACAGAACAGT	240
TGAATCTACA GTAACATCTA CTAATGAAAA TAAGAGTTAT AAGGAAGATG TTATAAGTGA	300
CAGAATTATC AAAAAAGAAT TTGAAGATAC TGCTTTAAGT GTAAAAGATT ATGGTGCCTG	360
AGGTGATGGG ATTCAATGAT ATCGACAAGC AATTCAAGAT GCAATAGATG CTGCAGCTCA	420
AGGGCTAGGT GGAGGAAATG TATATTTTCC TGAAGGAATC TATTTAGTAA AAGAAATTTG	480
TTTTTTAAAA AGTCATACAC ACTTAGAATT GAATGAGAAA GCTACAAATC TAAATGGTAT	540
AAATATTAAAG AATCAACCTT CCATTGTTTT TATGACAGGT TTATTTACGG ATGATGGTGC	600
GCAAGTAGAA TGGGGCCCAA CAGAAGATAT TAGTTATTCT GGTGGTACGA TTGATATGAA	660
CGGTGCTTTG AATGAAGAAG GAACAAAGC AAAAAATCTA CCACTTATAA ATTCTTCAGG	720
TGCATTTGCT ATTGGGAATT CAAATAACGT AACTATAAAA AATGTAACAT TCAAGGATAG	780
TTATCAAGGG CATGCTATTC AATTGTCAGG TTCGAAAAAT GTATTAGTTG ATAATTCTCG	840
TTTTCTTGGG CAAGCCTTAC CCAAAACGAT GAAGGATGGG CAANTCATAA GTAAGGAGAG	900
CATTTCAGATT GAACATTAA CTAGAAAAGG TTTTCTTAT GCCTTGAATG ATGATGGGAA	960
AAATCTGAA AATGTGACTA TTCAAAATTC CTATTTTGGC AAAAGTGATA AATCTGGGGA	1020

1343

ATTAGTAACA	GCAATTGGCA	CACACTATCA	AACATTGTG	ACACAGAACC	CCTCTAATAT	1080
TAAAAATCAA	AATAATCAT	TTGATAACAT	GAUGTATGCA	GGTGTACGTT	TTACAGGATT	1140
CACGTGATGTA	TTAATCAAAAG	GAAATCGCTT	TGATAAGAAA	GTTAAAGGAG	AGAGTGTACA	1200
TTATCGAGAA	AGCGGAGCAG	CTTTAGTAAA	TGCTTAAGC	TATAAAAACA	CTAAAGACCT	1260
ATTAGATTFA	AATAAACAGG	TGGTTATCGC	CGAAAAATA	TTTAATATTG	CCGATCCTAA	1320
AACAAAACG	ATACGAGTGG	CAAAAGATAG	TGCAGATWT	TTAGGAAAAG	TATCAGATTAT	1380
TACTGTATCA	AAAAATGTAA	TTAATAATAA	TTCTAAGGAA	ACAGAACAAC	CAATATTGTA	1440
ATTATTACGA	GTTAGTGATA	ATTTAGTAGT	CTCAGAGAAT	AGT		1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT	TTTTTATAAA	TATCATAAAG	CCAATCTGAT	TTATCAAGTG	TGTCTAAGCG	60
ACGCGAATTA	AAATTCATTG	CATCTCCAT	CGCTTCTAAA	AAACTCATTT	TTGAAAAGAC	120
GTTAAAAATCA	TCTAAATTCT	GACTCCAATA	TAATAACAAA	ACCAATCCCA	TAATATCCTC	180
TGGTTGATTA	TTCAATAAAT	TTAAGTTGGT	TTCATAAAC	CCTGGAGTTC	CAATAGAGG	240
CAACTTTT	TCTTCAATTT	GAGTTTCTTT	CCTTAGGGCA	TGCTCAAAGT	CTATAATATA	300
AATATTATTT	CTATTATCAA	TAAGTATATT	ATTAATGAT	AAATCTCTAT	AGGAAGATT	360
ATATTTGGAG	TTTATTATCT	CCATATAATC	AATTAATGTT	AAAAACCAAT	CATACGAGCC	420
ACTAACCATA	TTATACTGCG	TTAATTATC	TGCAATAATA	AACTCAAAAT	CCACAAAATA	480
CGAATTCCTT	ATGTAAAAAT	CGTTAAAAAC	TTTTGGAGTA	AATTCCTCCT	TTTCCAAATC	540
TACTAATATT	TCTCTTTTAT	TTATTAAACG	ATTACAGAA	TCTCTATTG	TAATCAAC	600
CAACGATAAA	TCACTAGCTT	CTTTTAATAA	AGAATAAACT	CGCTTTTGAG	TATTTAAATAC	660
TTTATAAACT	CCACCTTTGG	CATTTTATGA	AATCACTTCC	AAAATAATAT	ATTGATCAGG	720
AATAGTGTTA	TATCTTGAA	TATAGTAATC	CCTTATTGGA	ACATTCACAT	TTGAAGGAT	780
TTTCTTATCT	CTTTTATCCT	TGAAAGTGCT	ATCTTTTAGC	AACTCCCCAT	ATCTGTAATA	840
TACAACCTCG	CTAAGTTGAA	ATCTGAAATC	TGATGGTATG	TTTACACCTT	TTACACCTTT	900

1344

ATACAATATT TCTAATTGTT GTAACAAAGC TTGAACCTCT TTATTATCTT TTGGATAAAAT	960
TGTAATGAAT TTCCCGACTT GTGAATTAACC ATTAAGCCCT GTATTTTGCA AAGAAGGTTC	1020
TTTAATGCTA ACCAAAAATT TGAAATTTAT CTTCCTCTCT CTAGAAAAATA TAAATCAAA	1080
GAATTTTTTA GCAACCAAAAT TAGCATTTAA TATGTAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG ACGGCAAAAT ATATAACCAA TGTTTCATCAC TAAATTTATC	1200
ACTAATTTTA TATTCTAATA ATAAATTTATG GTATGGGTCT TCTATTTTCTG TTTCATAGTCT	1260
CAAAATAGTTT AAATACTTTT CGTAATTCAT ATTAAGAAAT CTCTCCATA AATTTTATGA	1320
CCATCATTTA AAGCCAAACA ATTTAAAGCG TGATAATAAA TGTTGTATAAT CAATGTAAC	1380
TTCAAGTCTC TATTCTGTAA TTCCCTTACC AATAATTTTA TGCTATATCT ATTTCTCGA	1440
GGCAATTTAT AGGACTTCAA GATAAAACCA TAAAGAGAT AAGTATTATA ATCTGACAAAT	1500
CCAGTTTTCAG AATAATTTTT TAGAAAAATA TCTATGTATT CTGATANTTC ATCCGGAATA	1560
ATTCTTTTGA CATCGTATTT ATTTTTCATA TCGGCCACTC TTCTTTAAAA AGCTCACAAAT	1620
AAAATTTTAA ATTTCTATAC AACAAATCCGA GAGTAGTCTC ACAATTTGAA CATTTCACAT	1680
CACCTCTTAAT ATATAAAAAA TGAATTAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACTTTCT ATATCATAGT AAGGAATTC ATATATCCCTA ATTGAAAAAT GAAATTTTAT	1800
GTTTTATATA TTAACAATTA TCCGGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCC CAGAAGGCGA TGCAACGCTA TTTTGAATTG AAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG CAATGCTTCC TTCTCTCTTC CGACAATTCG AAATTTTCTA	1980
ACTACCTTTT CAGGATTATC AAAAAATTCT CCAACAACCT CCATATTTCC TTGAAGTTCA	2040
TTCAAGAAAG CTTTCATTTC ACTACTCATT ATATAGCTCC TTTTCTATTA CTTAATTTGG	2100
AATCAAAACT TACTTGTACA TTGGAAACAC CTCTATTCTA CGCTTTTATA TTGCTGCATG	2160
ACACTTCCAA AATCAAAATG CTAATAATAA TTTTTTAAG CTTAATTTAG ATTTAATTAC	2220
ATATATCTCA AAAAAATTGT TTGAATTAG TAAATTAATA TAGGTTTCTG TACTATAGG	2280
AACTAGTTAT AAAAACTTCG CCCATCATAA AATATCTATT TAAGTAAAC AAAAAATTTA	2340
TAATTTTTTG ATTTTTAAGT GACTATAATC TCCTATCTAT AATACCANT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT CTTATGAAC TGAGTTCTCTC CAGACATCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1049 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

1345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAAATTGAA GGCTCTAAAA CAATGAAAA GTGCTACACA GATGTGACAG AATTGGCCAT	60
TCCAGCAGTA CTCAAAAAC TTAATTATCA CCAGTTTATG ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTTA ATCTTCTCTG TTGCGCTAAT TTAGAATAAG TACAAACAAAT GTTGAACAG	180
GCATTCAAAG AGAAGCACTA TGAGAATACG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCTTAGAG AGTAAGGGAA TTCAAGCATC CATGTCAAGC	300
AAGGGCAACA GCCCAGACAA CGCGATGATG GAATCTTTCT TTGGCATTTT GAAATCGAG	360
ATGTTTTATG GTTATGAGAA GAACCTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTAA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCGGATAA ATTAATTGTC TAACTTTTGG GGTGCAGTAC	540
ATTTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAACT TACTATATTC ACAATGTTAT CCAGTGTCTT TCTCTAATA TTTAAGGAGT	660
GTCTGTGTTT TCGAATAAAT TCTTCAAGT TTAACCCGTC AACTGTGTTT TGAACAAGAA	720
AATTAATCAT CACGATATAA AATTCATCAG TTAAATTAGT AGTATACTT TTATCGGCTA	780
ATTTTTTAGC CATGTAGGCT TCATTTTTTA TATCATCAAG AGCTGTCCAT TCTCCTTCAG	840
CATCAATAAT CACAAAAGGT CTGACTGCT TGATGATTAC TTTTGGCCCG TCOGATTTTC	900
TAATGCGCCG ATAAACATTT CCTTTATTTG ATCTCTTAAT AATTTTTTCC ATTTTGTATT	960
TATTTATGTC AGAGTCCTTA CTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTTT	1020
CTTCTCTGTA AATAAATCC ATTTTCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAATCAGAA AATCGCGAA GTGGTTATTT ATTTTGAAT AAATTAAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTCAAC AATTAAAAAA TTATGCTGAT AATACAAAA	120
TGAATCCTAA AGTAATTAC CCTCATCTT TTAGGCATTT ATTTGCTAAG AATTTTTTAT	180

1346

CGAAGTATAA TGATATTGCC TTGCTTGCAG ATTGTATGGG ACACGAAAGT ATAGAACTA	240
CTCGAATTTA TCTAAGGAAA ACAGCTACTG AACACAAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAA AATAACAGGT GGTCAAACTG ACTACCTGCT MTTTTCGTGA TTATGGCTCT	360
TATTTATGGGA ATATACCTAT GAATTGGGTT GTTATAAAAA TAAAAGATAT TTTTCAATA	420
AATACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATTA NTAATAAAGG TGTTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTACTACATT	540
GATACACAA TCACTCCTCT TGAGCAAGTT TATTTAAATC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTTAGAACA TATTGGAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTGTGGCTG GTGGATGTAT TTTCCAATTA ACACCATTCG AAAGTCGAGA GATGATGTCA	720
AAATGTCTAT TATGTAACCT GTCCCTCCG TATTTTATA AACAAATTGAA AGCAAT	776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCGCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTTCGATC AGGATGATCT	120
GGACGAAGAG CATCAAGGGC TCGCGCCACC GAACGTGTTCG CCAGGCTCAA GCGCGCATG	180
CCCGACGGCG AGGATCTCGT CGTGACCCAT GCGGATGCCT GCTTGCCGAA TATCATGGTG	240
GAAAAATGGC GCTTTTCTGG ATTCAATGAC TGTGGCCGGC TGGGTGTTCG GGAACGCTAT	300
CAGGACATAG CGTTGGCTAC CCGTGATATT GCTGAAGAGC TTGGCGCGCA ATGGGCTGAC	360
CGCTTCCTCG TGCTTTACGG TATCGCGGCT CCCGATTCGC AGCGCATCGC CTTCTATCC	420
CTTCTTGACG AGTTTCTCTG AGCGGGACTC TGGGGTTTGA TGTTCAGACG CCGCTAATG	480
AGCGGGCTTT TTTTCTCTGA GGCTGGACGA CTTGCGGGAG TTCTACCGGC AGTGCAAAATC	540
CGTCGGCATC CAGGAACCA CGAGCGGCTA TCCGCGCATC CATGCCCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGTCTCC GGATCAATTG GCCTGACCGG ATCGATCC	658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1475 base pairs
 - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT TTTTAGAAAA CGTGGGCAGG GAACCTTTGT TCTCTCTCGT GGCAGCTCAA	60
AAAGAAATTT AATCGTTCCA GAAAGAGATA TCCGGGGACT GACAAAAATA TCTGAAGATG	120
CTCATCTAC AATTGACTCG AGGATTATTCT ACTTCAAAT AGAATTTGCA AATGAATTTT	180
TAGCAGAAAA ACTACAGGTC GCTTTGCAGA GTCCAGTTTA TAATATTTAC CGCCTGCGTA	240
TTATTGACGG TAAACCTTAT GTTCTGGAAC AAACCTATAT GAGTACCGAT GTTATTCAG	300
GTATTACTGA AGATATTTTA CAAAAATCGA TTTACAATTA CATTTGAAGGA AAGTTAGGAT	360
TGCATATTGC CAGTGTCTACA AAAATCTTAC GAGCTTCTTC TAGTTCAGAA AATGAGCAAC	420
ATTACTTGCA GCTCCTTCCA ACGGAACCGG TATTGGAAGT AGAACAAAGTG GCTTATTTTG	480
ATAACGGAAC TCCGTTTGAG TACTCGATTA GTCGTCATCG CTATGATTTA TTTGAATTTA	540
ATTCTTTTGC ATTACGACAT TCCTCCTAGG AGAAAAATGT AAAATGAAGC CAATCTTTTA	600
CAGACTCTAG TTTAAGAAAA ATTTAAAACA GGGCAAGAAG GTCCCATCTA TGCTTAAATG	660
GTTCCTCTTT TCTAAATAAG ATGGCTTTAA AAGAGTGAAT GTTGATCCA TCATGTTGAA	720
AAATATCTTC GTATAGCTTA TAGAGTAGGT ACTGAAATTT TTCACCTGAT CTACTCTTTA	780
TAGTTATTTA GTTTTAAATA GTGTTTCAAA CATTTTACCA CTGACGAGAA GTTTTGGAGT	840
CTTTCTTGT AACACATATA GTATACTGTG GTTAGAATAG TAGACTGTGA CTTCATAACA	900
ATTGCTAGAA ATGAATTTCA ATCTCCCAAT TTATTTGTT ATATCTTCTT TTAATATATT	960
AAATAAATTC TAAATCATAA TCATTTAAAA AAATTTIAT TTTTATTTT CATPACGAAT	1020
AATATAGATG AAGGGGAAAG AGTATGAAAA CAGAACTGTT TCTTTTGCTA TTAGTTCAAA	1080
AGGAGAAAAA ATGAAAGTAG AAAATATTTT GTATAGGGTG GATCATCGTA AATTGTTTGA	1140
TAATATTTCT TTTGATACTT CGAGTTTACA CTGACATTA ATTACTGTA AAAATGGTAC	1200
AGGAAGTCA ACTTTACTAT AGTAGATTGA AACTAGAATA GTACACATCT ACTTCAAAA	1260
TATTTGTTAG AATCGATTTG ACTATCCTGA TCTATTTGTC CTGTCCTTAT TTCAATTCAC	1320
TATATCTCAA ATGAGATGAT ACGAAGTGGC CTCCATGTCT CTGGGAACGC ACTTTCTTCA	1380
TATTTTTCAT ATTCTTGAAT CCATCGATAA AGACTATTGG GATGAATTTT TAAAGTTGAA	1440
CTAATCATTT TTACACGATG AGATTTCACG CAGAG	1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACATA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATAA CCACATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTT GTGCGGGTT	240
TGAATTTAAA AAATTTGTTA TGTAGTACCT AATCTAAGGA ATTAGAACA TGCTCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGAACA AGCTCTCTT	360
TGCTCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTC CTAACGCTAC TTGAGTTTT	420
TTTCTAAAT ATTCTTTTCC GTTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAAFACTCT GGGTTGGGA AAGGAAGATA AGAAACGTAT	540
TTAGCCCAT ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CGCCCGGCC ACGCTGCCT ATCCTCGGA GAGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCCTACTACT TTGCGGACG GCGTCGTCG TTGTCATCCA	120
CGAAGTATC GGACATGGGT GCGAACACT CAGAGAAAA ATCGTTGGAC TGCCTGTCGG	180
GCGTAGGAA CTACGGGTGG TGGCTTTTCC GAAGAACGGC TCGGGTTTG ATGACGAGGG	240
TACACCTTC GAAGAGATTG TACTTGTGA GAACGGCATT GTGAGGCACG CTGTACGGGA	300
TCGGGGACT GGAGGAATGG GCCTTTTTTC CGGTTTGACC AAAGTGGCAT CACATGTTGT	360
CAACCTGCG TCAAGATGTA CGCATCTCAA GCGGGAAGGG GAATCGTCAC AGGAAGGAGT	420
TACCGGAGTA CCCGCGAAC GCACCGTTTG GATAGAGCAT TTTCTGTCAG CGAACTACCA	480
TTGAGGTGCA GCCTTTTTC GGTCTGGCCT TGCTGGGTA GGCAGCCGAG AAGAACTCTT	540

1349

ATATCCCTTA ATGCCCTTCA CGATGTCAAT TGATATCTAC GAACTGGCCA GCTTATTTGG 600
GCATTAGAC GGTCAAACGG AACGAGCAG TAGGGTACTG TGC 643

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTGAT GAATTGTGAA CAGTTGCCCT TGGGTGGTTT TGCAGTTGA 60
AGTCAAGAAG AGGAAAAA CAAAAAGGAG AAATACTCAT GGCAGTAMT TCAATGAAC 120
AACTCTCTGA GGCTGGTGTA CACTTTGGTC ACCAACTCG TCGCTGGAAT CCTAAGATGG 180
CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTAT OGACTTGCAA CAACTGTAA 240
AATACGCTGA CCAAGCATAC GACTTCATGC GTGATGCAG AGCTAACGAT GCAGTTGTAT 300
TGTTCTGTTG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAACA GTACGTTTCA 360
GTCAATACTT CATCAACCA COTTGGTTGG GTGGAACCTT TACAAACTGG GGAACAATCC 420
AAAAACGTAT CGCTCGTTTG AAAGAAATTA AACGTATGGA AGAAGATGGA ACTTTCGAAG 480
TTCTTCTTAA GAAAGAAAGT GCACCTCTTA ACAACAACG TCGCGCTCTT GAAAAATTCT 540
TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTALTG ACCCACATAA 600
AGAGCAAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCACTTGTAG CGATGGTTGA 660
CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG 720
TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT 780

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 624 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGAAAAAT CAGATTGCG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAT 60
AGGTGTCGAA TTGGAACATAT CTCCCATGAG TTITGATAAT GTACTGGCTA GTGTTCAATC 120

1350

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	180
TGACTTTTCC ATTCCTACT ATACTGCAA AATAAATCTC ATTGTCAAAA AATCTGACTT	240
GACTACTTAT CAGTCTGTAA ACGACTTGGC GCAGAAAAAG GTTGAGCGC AGAAAGGTTT	300
GATTCAAGAG ACGATGGCGA AAGATTTCCT ACAGAAATCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGGAAT TTAATGCACG ATTTAAATAT AGACAAAGTG GATGCCGTTA TCTTTGAAGA	420
ACCTGTTTCC AAGGATTTTG TGGAAATATA TCTGTATTTA GCAATCGCAG ACCTCAATTT	480
TGAAAAAGAG CAAGATGATT CCTACGCGGT AGCCATGAAA AAAGATAGCA AGAAATCGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGGAATTA GACAAATCTA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAAGCGTG ATTTATGGCG GATAGGTTTG GTCTGCAGAA AGTGACAAAT	60
CTAGTGCAT CAGCGATAT GGAATCTnTG GCTGAGAAAC AGTCCCGGGG TGAAC TGACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC	240
AGTCTCGCA TCTTACTTGC TATTCAATAG GAGTTGTTTC AAGATATAT TGAACCTCG	300
ATTCCGGTAG GTCAATTTTG TCAGACTAAT ATCACAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTACTCCATG ATTCAAATGA CCTTGGATTA TGATTTTAAT	420
CAGGAAAAAC AAGTTGCATA TCGACACTA ACCCAGGCGG ATATGGTTAA AAAAAATCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCAAT CCATTTCCGC AAGGAAACAC TCGGACCGTA	540
ACGGTATTTT TGATTCAGTA TCTTCTGTAG TTTGGTTTTC ATATTGATAA TACACCATTT	600
CAGCAACATT CCAAGTATTT TCGTATGCC TTAGTGTAG ATAATGCAAA GATTTACAG	660
CGACGCTCTG AGTTTAAAC AGCTTTTTTT GAAAACTCT TGCCTGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAAATGTA TCTAGATTTA GACCTCGATC TTTCATAATC CTAATATGA	780
GTAACATTTG AATTTAGGA AAAAATGAG TAAATATTCT CACAAGAAA GATATATCAT	840
CAAAGTTTGG CTCCTTGTCA ATTTGATGTG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTTCGGC CTTTCCTTTT TGATGTTGAG AGCGATATAA ATCCGGTTTT TTGAAGTTTT	960
CAAAGTTTCG AAAACCAAG GCATTGCGCT TGATAGTTTT GATGAGATTA TTGGGGCGCTT	1020
CCAGTTTGGC ATTAGAATAG TGIAGTTGAA GGGCGTTGAT AACCTTTTCT TTATCTTTGA	1080
GGAAGGGTTT AAAGCAGTC TGAATAATAG GATGAACCTG CTTAGATTG TCCTCGATAA	1140
GTTCGAAAAA TTTCTCGGG TCCTTATCTT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTTT CTGAATTAGA AGAGATTGAA TTGCGTCAT CTCTAGAATA TATTGGAACA	60
AGTGCAATT CTTTAGTCA AAAATTGAAA AGCTAACCT TTTCTCAAG TTCAAAATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAAAT TAGAGAACT AACATTACCA	180
AAATCGTTA AACATTAGG AAGTAATCTA TTAGACTCA CTAAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTTGGC TCAGTTGATG GTGTTTTGTT TTCAAAAGAT	300
AAAACCAAT TAATTTATTA TCCAAGTCAA AAAATGACG AAAGTTATAA AACGCCTAG	360
GAGACAAAAG AACTTGATC ATATTGTTT AATAAAATT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTAGAAAA AATCGTACT TTGCAATTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTTAACAAT	60
ATATCAACA TCAATGACTA GAATACTGTC ATCATCCTTC TTTCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAATCTCA TCTTAATTA CTCCTCAAAA GTTTTATTTT GATTATTTTG	180

1352

ATAGAATTCA TAAAGCCAT CGCTCATTAA AACAAITGT TCACTAGTAA CATCTATTTG	240
ATTAAATAATA GCATGCTCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTAGAT AATTTTCGA TTTTTGTAA AATAATTTT TTATTTAAAA CACTATTTGT	360
ACCAATTGAA TCTTTTATCT CATTTTCCC TTTTTCAAAT AAGTTATCTA CTCATGATC	420
AGTTATTTCG ATTTCGTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACCT	480
TTTTTCGAA AGTTTAGCAA ATATTGTGTA GCGATATAT AGTATATTGA AACTAGAAATA	540
GTACACCTCT ACTCTAAAA CATTGTTAGA AATCGATTG ACTGCTCTGA TTGATTGTGTC	600
CTATTATYAT TTCATTTTAC TATACTCTCT TAATTTATAT GAGTTTAAAC CGATTTTCATC	660
TTTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTTAAGA GTTTTGTATT CTTTACAAAT	720
AACCGACAAA CTTTCTGATA AAATATGTAC AACTCTGAG ACTGAAATAC CTATCTCCTC	780
TTTAGAATCA TATAAATCTG TAGCTCCACC AATAATCCAA AAATATGAT TTTGTGAACC	840
TACAATATCC TCATTTCTA CGGAACCTCC TTGTATCGAA CAAATTTTAT TTATCTTTAC	900
CATAATACTT CAACCCCTT AGTGTCAAAA GTAAACCAAT TCCTGTCACT GTTAAGAATA	960
GTTCATAAT CTTATTCGAA CCACTCTTTG GTAAATTTTG TTTKACATCT ACTATYCTT	1020
TAGATTATAT AATATGATT TCAGTTTCTC TGCCATCTCC AACTATTTTA TAGTTTACTT	1080
CTCTGTCTT ATTACTTTGT TTATTGTGTA TCTGTCAAT CATTTGTCTA TTATCTTTAC	1140
TTGAGTTAAA CTCCTCGTTC TCTCGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCCCTCTT GTTTTCTTCT TTTTCGTTT TATCACTTAA ATTATTTGTT ACAATTTTGT	1260
AAAGCCCCAT CTCGGTTACA ATATTGAAAT TACCATCGCT ATCAGGATA ACAGTTTCTT	1320
TCCCATTGC ATTAGATTG ATGAATGATA TATACTTACC GGATAAATTA TAAATTTGGT	1380
TATTTAAAAA GGTATTTTAA CCTTTTGAAT COTCAATAAC AATTCTCTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 646 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAMATCA ATCTCAAAATG GTTCGTCAAT GGTTCTGTAT	60
ACCTATTTTC COTCTTCTT CCGTGTCTG ACACACTCTG TGAGGAGATA TTCATTTTGC	120
CCATTGACTG AACGAAAGTC GTCTTCTGCC CATCATGCGA GTACAGGATA TAACTTTGTT	180

1353

GAGAGTCGAA GGGGATCTG CTTTTTTTA GCTTCAGCCA TCCTTAGTAA AGGCTTCCTG	240
TGTTGACAAAT TGCTTGTCGA TCATGATTGC CACAAAGAAC GACAAGGAGA TTTGAAACCA	300
TGGCAGCTTT TCCTTCTTGC TCAAGTTCTA CCAATTCCTC TTCATTGAGC CGTTCTAGTG	360
CCATTTCAAC CATTCTTACA GCACCACTA CAATCATCTT CCGTGCATCA ATAAATGCGAG	420
ATGCTTGTTG GCGTTGAAGC ATACGGCAG CAATTTCTGG AGCATTAAGT AGGTAAGTGA	480
TACGTGCTTC AAGGATTTCC AAGCCAGCAT CCTCAACACG ACTTTGGATT TCCTCACGAA	540
TACGGTAGC AACAAATTCG CTAGAGCCAC GGAGACTACC TTCATCTGCG TGCCCATCAC	600
CCGAGATATC CACATTAGGA GACACATCGT AAGGATAGAT GCGGAC	646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTCAGGTG CAGTAGGTGT TACTTCAGAT ACATTTGAAC GTGCAGAAGC TCTTTTTGAG	60
GCAGGAGCG ATGCGATTGT TATTGATACT GCACATGTC ATTCTGCAGG TGCTTGCCT	120
AAAATTGCCG AGATTCCTGC TCATTTCCCA GATCGAGCTT TGATTGCTGG AAATATTGCT	180
ACTGCTGAAG GTGCACGTGC CCTTTATGAA GCGGGTGTAG ACGTGTGTAA GGTGGTATT	240
GGACCGAGTT CTATCTGTAC TACTCGTGTG ATTCCTGGTG TTGGTGTCC GCAAGTAACA	300
GCTATCTACG ATGCTGCAGC TGTTCGCGCG GAATATGTA AAACGATTAT TGCTGACGGT	360
GGGATCAAGT ATTCTGGAGA TATTGTAAAA GCACCTTGCTG CAGGTGAAA TGCTGTTATG	420
CTTGGATCTA TGTTTGTCTG AACTGATGAA GCTCCAGCG AAACGAAAT CTCCCAAGGA	480
CGTAAATTCA AGACTTACCG TGGTATGGGA TCAATTGCTG CTATGAAGAA AGGTTCAAGC	540
GACCGTTATT TCCAAGGTTT TGTCAATGAA GCAACCAAGC TTGTTCCAGA AGGAATTGAA	600
GGTCGTGTTG CTTATATAAGG AGCGGCAGCT GATATTGTTT TCCAAATGAT TGGTGGTATT	660
CGCTCTGTGA TGGGTTACTG TGGTGCAGCT AACCTTAAAG AACTACACGA TAATGCTCAA	720
TTTATTGAAA TGCTCTGTCG TGGTTTGAAA GAAAGCCATC CTCATGATGT GCAAATTACT	780
AATGAGCAC CAAATATTTC TATGTAAAA ACAATGAAA GAATCCAGT GAAACAGGA	840
GTTCTTTTAC AATGTTGTCA ATTTCATT ACAGCAGCTT TACCATCTG AATAGTGAAG	900

1354

ATACTTAGAT TTTCTGGCAG ATTTTGAAGA TGGTCTAAGC TTGTTGTGTG GATAAAGGTT	950
TGGATTGATT GAGAAATCGT TTCTAATAAT TTTAACTGTC TAGTGTGTGC AAGTTCACTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCCTTCCAT TAATTGATTT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTYGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCCTT	1200
TTAAATAAAT CTCTGGATCT ACTTTTTTCT AAAGCAATTT TGAAAGATTC GGATAAGTTT	1260
TGTTTGTGAG TTATAATTGAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAG AATGTTTCTT ACGCCCAAAAT GATTCTAGTT TTTTATGAA ATCTAAGCGG	1380
TGATTCATTA CACGACATCC ATTAATCACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTAATT TTGAGCTGA TTTTAGGTAA GTGTTTCTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATTGGCTTA ATTTGCCCAA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAAATCTT CAGGAGCAGA TAAGACAACA	1620
TTTCATGTCT CTACATAATC TGAAGGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTCAAAGC ATTTTTTGT AGTTTAAAT TACTCCCAAT CTCTTTTCC	60
AAACGTACA TATATCCAAA ACCATTCAAA ATACTAGATT CTATTTTTTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTTCAGA TTTTGTAGTCC CAGTCCCACT ACCGAGAGAA	180
TATTGTTTTA ATATAATATC TCTTTTGTCT TTCTAAGTCT TTAAAAGCAA AAGACAAGT	240
AAAGAGTCAA GACAAGATA AAAAGTCCAT ATTAGGCGAA ATAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAGACCA TAGCAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCTTTAT TTTTATATCC ATTTTCAAAA TCAAAATTAT TCAGACTATA	420
TATGCACATA TACACTTAAA TTCAATATAA AACATGGCTT GTAAAAAAT ACTTTAATCA	480
CAATAAATCG ATTTAAATTT GTGATGTTTG CAAGCTAAAT TACGGACTTC ACTTGAAGT	540
TTTCCCTTGT ATCTTTTATA ATAGATAGAA AATTGTCTGG CAGATGAATA TCCACAGAT	600
TCTGCTATCT CTTTATATAGG TAGTTCACTG TTTAAAAGAA GAGTTTCAGC TACATTCATT	660

1355

CTTTTCTTTT GAGTGACTC TGTAAATGCTT TGACAATAT TTTCTTAAA TAAATTTTTT	720
AAATTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTAC ATTGCTTGCA	780
AAATGATCAT CTAAGAATCT TGCATCATCT TCAAGTGTCT TATCATCATC AATTTCAATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCTTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAAA	1020
GATTCGGAT TAATGTTAAT AGATGCTAAA TGTTTTCTTA TTAGTCTTTT TTTAAAACm	1080
ATGGAACACG CAAGATAACA ACAATTCCTG TGTATAAAA AACAAAAAT ATCTTTTATA	1140
TTATCAAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAACTTGAA TAAATGAAA CATAGTCTGA CATACTATA	1260
GTGCTATTTT GAACACTCTC CTCTTTTGATA TAAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGTA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTGT ATGAGTTTTT AAGTAGGAAA AACGTCTAA CCTCTCAGAT TTTGGAACCT	60
GTAAGAAGAA CTCCTTTTTC ACCCGTAGTA GTTGATAATG GGTTCGATCC GGCTTTATTT	120
GAATTTGAGA AAAACAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT	180
TTTGCACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCCTCA ATTGGAATAT	240
AGTGATTTAC GAAATCGTAT TTTAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTTCG CCAATGATCG AATAGATTTC TTTTCTCTAG GTGATTTTAA TGAGGTTGAA	360
ATTCAAAATG TATTAGAATC ATTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTTCAG	420
TATTGTCAAC CTATTCTTAA TATCTTTCAG GAAGGTATGG TTTCGAAAAA TGTGGGACAA	480
TCCATTTTGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGACGA ACATTTACCC	540
ATGGATTGAA TGAATGCTTT ACTTGGTGGA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGAAAA	607

1356

(2) INFORMATION FOR SEQ ID NO: 332:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAATACC GAATTTTGT TTGTCCTCTA TTCAACATT GTGAATCGCC TCAGGCAGAG	60
AACCGATACT AAGATATAA CCAAAATAGT TGTCAATTGC TTACCGATA TCAATCTTAT	120
TGGTTAAATC AAAATCCAGT TCGTCAATTG CGCCATCGAT GTCTTGATG ATTTCCAAAA	180
GTTTTGTAAAT GAGGTTACCC GTACCGCCTG GGATAATCCC TAACTTAGGA ATGTAGTCTC	240
TCTCATCAAT ACCTGAAATG ACTTCATTGA CAGTTCATC TCCACCAAC ACAACCACTG	300
CATCATACTG CTCACGAGAA GCTTCCTCAG CAAATGTGT TGCATCCAGC GCTTTTTCGG	360
TAATTTTGGT TTCAACATAT TCAAGTATT CTTTGTCTT ATTCCTCAGC TTTTCTTGT	420
AATCCAAAGC CTCTCGCCA CCAGAAAGTAG GGTGATAAT TACCATTGCT TTTTTCATTG	480
ATTTATCTCT TAATTTTAAA CAGAAATGTT TACATTTGCT CGTATGCAAG TAAATGTAA	540
CCTATTATAC AATGAAAAA CAGAAAGAG AAATCTGACG TACTGGAGAT TAATACGCTT	600
TTATTCTATT TTCCATCGC CTAATACAT CCTTTAAGGG TTCATCCAAG TAAGAATAGG	660
CCTATCTCTT GATCCAATCA GGAATACCGT AAGCTGCTC TGCTAWGCTA CAAGTGATTG	720
CTGCGAGAGT ATCACTGTG CCAACCAAGT AGATGGCATT TCTTATCGCA TCTCGAAGT	780
CTCTACTTTC AAGAAAGGCG ATAAATGGCTT GAGGGACAGT TTCTGACAT GTTTCTGTAA	840
AACGATAGTT AGGACGGATT TCATCTAAG TTTGAGATAG ATTGTAATCG TATTCTTTTT	900

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGCG ACCTGTGCTT TGGAAACGG CAAACCTCT GAAATATCT ATGCTGGAAT	60
GGACGAGGAA TACCGTCGTT ATCAGCCTGC CATCATCACT TGGTACGAA CAGCCAAACA	120
TGCTTTTGTAT CGCGGACAGA TTGGCAAAAT ATGGGTGGAA TCGAAACGA CCTCAAGGC	180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATG AGGAATTGCG TGGTGAGTTC	240
AACCTGCCAA CTAATCCCTT TTACCACTC TCCAATCTGG CCTACACTCT CAGAAAGAAA	300
CTGCGCAGaA GcATTACAG AAAGGAAGCC TATGACCTTT AAATTCTCA GCCAAGAAGA	360
ATTCAATCCAG CATACTCAG CTAGATCCCA ACGCTCTTTT ATGCAGACCG TAGAAATGGC	420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGS	480
GAAGGTAGTG GTGTCAGTG TCCTCTACAG CATGCCTATG ACTGGTGCC TTC	533

(2) INFORMATION FOR SEQ ID No: 334:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID No: 334:

CCAGCAAACT AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTTGAGGT TGTAGATAAG	60
ACTGACGAAG TCATGTACAA AACACTGTTT TGAGGTTCGA GATAGAAGTG ACGAAGTCAG	120
TCAAAACACT GTTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAAA CACTGTTTTG	180
AGGTTGCAGA TAGAACTGAC GAAGTCanna ACCACACCTA CGGCAAGTG AATCTGAAGT	240
GGTTTGAGA GAGTACAACT TGCTTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC	300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTA TCTTGATGGA ATCTTAGCAG	360
TCAAGGATTC TCAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTTA GAGCAAGCTG	420
AGCAGATTAT AGACTATCAG GGAGCTTGA TTAATGCTGG TTTGGTCAAT TGTCACACCC	480
ATTCTGCAAT GACAGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA	540
ATGA	544

(2) INFORMATION FOR SEQ ID No: 335:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID No: 335:

CCAGGAATC AAATGTAAGT AGGGGTCCT TTTTGTATA TTTTCAAAT AACGCCTCTA	60
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1358

CACATATTGT AGCAAAATCA CCAACTACAG TTGTATCTTA GTTAAATAA GTTAGAATAT	120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCACTT AAGGTATATT CAAAATACAA	180
AACCTCACCA ACTAGATTTC TGAATATCCT TATATATCCA TTCTTAAAT TGOTTTAAAT	240
AGCCTAGTCT TTAAACTAG TTTTGAGAAT CCAAAAAATC TTCTACATA TGTAAGAAGA	300
TTTTTTACTT CAGAAAGATT ACCTTTAGCT AATGGATACC TATCCTACC	360

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAC CACACAGCA ATGGAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAAATTTG AATCAATTTC GTGATTGGTT TCTGACGCTA	120
AATTTCAGT TCAAGTTAGC CATCAAGAAG TCTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTAGGAT AGTGTAAAT CCACCTTTTC ATGAATGCGA CTCTTTGGG AGTCATTTTC	240
TTGGTTCCCT TAGGTAACCA TCTACGAATG AGCCTGTGT GATTCTCATT AGTCCCGGG	300
ATCTCTAGA GTGACCTGC AGGCATGCAA GCTTGGCACT GGCCTCGTT TTACAACGTC	360
GATGACTGGG GAAACCCCTG GCGTTACCCA ACTTAATCGC CTTCAGCAC ATCCCCCTTT	420
CGCCAGCTGG COTAAATAGC AAGAGGCCCG CACCGATCGC CTTCCCAAC AGTTGCGCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTCTCTCTT ACGCATCTGT GCGGTATTTC	540
ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCCG CCAACACCCG CTGACGCGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAATTTT CACCGTCATC	720
ACCGAAACGC GCGAAACGAA AGGCGCTCGT GATACGCTTA TTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTCTCTAGA CGTCAAGTGG CACTTATCGG GGAATGTGC GCCGAGACCC	840
TATTGTGTTA TTTGTCTAAA TACATTCAAA TATGTATCG CTGTTGAGAA AATAAACTTG	900
ATAAATGCGT CAATAATATT GAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCCG	960
CCTTATACCC TTTTTTGGG CATGTTGCCT TCCTGTTTTT GCTCACCCAG AAAACGCTGG	1020
TGAAGGTTTA AGATGCTGAA AAATCATTTG GTTGCAACAC TGGGGTTACA TCCAACGTGA	1080
ATCTCCACCA GCAGTTAAGA TCCCTCTGACA GTTGTACACG CCCCAAGAAC TATTCGCCAT	1140

1359

GAATGAGCAA CTTTAAAAAG TCCTGCGAAT GTTGGGGGGG TAATAATCCC CGTGTGTAG 1200
 GCCCCG 1206

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTTCTGAC TTACCAAAA GAACCATCAA AAAAGTTGCT 60
 GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTGGCCCTT ACCGTATGTC AAAAGATTTT 120
 TACCGTGAACT TGGGCTTAGA CACTCCTATG ATTAACCTCA ACGGATCCCT TACTCAITTA 180
 CCAGACCAAG TTGGGATTT TGAAAAAGTG TTGACTGTAG ACAAAAAATA TCTGCTAGAT 240
 ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA 300
 TTCTACATTA CAAATCCCAA TGAAGAAAT GCCAATCCCA AACTATTTGG TGTAGAAGCT 360
 TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCTTAA CTGTATCCTC 420
 TTGCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCACCAG 480
 CATCAACTTT CTATCAATAC CTGGGGAGGT CCGTCAATA TCCTTGAATG TACCCCAAAA 540
 GGTGTCAACA AGGCCTTTGC TTTGGACTAC TTGCTCAATA TAATGAATCG TGACAAAAAA 600
 GATTTGATPG CCTTTGGAGA TGAACACAAT GATACGAAA TGCTCGCTTT TGCTGGGAG 660
 GGTATGCCA TGAJAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTTCC 720
 CTTACCAACG ACCAAGATGG GGTGCCAAA ACCCTACAAG ACTTATTCCT ATAACCTATA 780
 CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA 813

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAAT TAAAAGGAGA TTGATGATGG 60

1360

ACAAATTATT TAACTAAAA GAGAACGGTA CAGACGTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACTTT CTTTGCAATG AGCTATATTC TCTTTGTAAA CCGACAAATA CTTTCACAAA	180
CAGGAATGCC TGGTCAGGGC GTCTTCCTAG CGACGATAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTATGCT AACCTACCTT ATGCCAAGC GCCAGGTATG GGACTCAATG	300
CTTCTTTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCGCTACCTA	360
TGGTCTTCAT CTGTGGGATT ATTTCAATGA TTATTTACCTT GACAAATGTT CGTAAAAATGA	420
TCATTGAATC GATTCCCAAT GCTCTTCGCT CMGCTATTTG AGCTGGTATC GGTGTCTTCC	480
TTGCCATGCT AGGGAATAAG AATGCTGGAC TTTTGAATTT CACGATGAT CCAGGCAACT	540
ATACTGTTGT AGGAGAAGGG GCTGACAAAG CTCGAAGCAAC GATTGCAGCA AACTCTTTCAG	600
CAGTTCACAG ATTGGTCAGC TTTAATAATC CAGCTGTTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTCTTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTTACA TGGAAAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CTTACGTTTG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGCTGTGTC TCTCATAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTT CACCAGTATC GATTATTTAA	240
TTATTTTAAAT TATTTTATTT GCACAGCTAT CACAGAATAA ACAGAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGGCGAG TTGATTTGCT GCTTATGTG	360
TTAATTTGCT GCCTGAAGAA TGGATGGGTG GATTGCTTGG TTTAATCCCT ATCATTTTAG	420
GGATTGCTT TGCATTTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGACA AAGCAAGGCA AATCAACTGT TTTGGAAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTATAGT ATCTATATAC CTTATTTTTT TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTTGCTTGIG TTGTAAATCG GCATAATTAT CTTTTCGGAG ATTAGTCGGG	660
TGTTATCCTC TATTCGTTA ATATTGAGA CAATTGAAAA ATACGAGCGA ATCAATTGTG	720
CCTTAGIATT CATTCTACTT GGACTATACA TCAATGATGA AAATGGCAGC ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT 840
CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA GCGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTAATG 60
GATAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120
CACCOCGCTT AGGTAACAA TTTTAGCAAT CAGATAAAC CAAAACATCA TAACAACAAG 180
AAGAACGGAA CCTAAATTC GGACATCCAC CAATGATGG ACATAGTAAT TGAGATAACT 240
AGAGAACAGA GTTAGTAAC CTAAATCAC TAAGAGAACA AAGGCACTGC CTGGTAGGGT 300
ATAGCTAATT TTCTTGTTAG ATAGATTGGG AAGAAATAA TAAAGCATGA CCAAGATAGC 360
AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCTTGT AAAGCCTGAT AGATAATGCC 420
ATCTTTTGTC CAATAATGAG CAAGTAAAGC CAAATCCTC TGACCAATAA AGATCAAAAA 480
CAAGGCAAC GCMAAGAGGA GCTGCAACCA AAATGACTA GGAGACTTAG CATCTGATGG 540
GAAATAAGTC CACGACTCTT TTCGACGCCA TAAGCCTTGT TAAAGCTTT TTGCAAGAAA 600
TTCATAGATT TTGAAAACT CCATAACGCC GATAAACAG AAAAACTCA TAAACCTGTT 660
GAAGGTTCG TCAGAACTTC TCTGGCTATT TTTTCCACAC CTTCATAGAG GCTTGGGGGG 720
CAGACGTCCT TCATAAGCC CAAAAATCT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 707 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATACT CTAGGATGAC CGCTATTACT CGACTTAATG AGTGACAAAG AAGTCAGGAT 60
TTTTATCGAG GTTGGCGCT TCATCAGACA GGAAGATT ACAGCGACTA TTATGGAGAT 120

1362

CAAGGTTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC	180
TTTGAGTGTG TAGCCTTGGT AGCAGGAGGA TTTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT	300
CTTGCTTTTG GTGGAGGCTA TGGGACTCTT TTAGCGCTTC CTTTCTTATF CGCAGGCTTT	360
AGTTTAGTTG CCGCTTACCT AAGCAATCCA AGCCATGATA AGGAGTTTGT ACGGATTGGG	420
CTAGCTTTGG CAGGCGGATT TTTCTTTGCT CCCTTATCAT CGTCTCTGTT TATTGCTGTA	480
GTGAGTTTAG GCTTTTGGT CTTTAACCTT GGGCATAGAC GCTTTGCGCA TGGGTTTTAT	540
CAOTTCTCTG CAGTGGCTTT AGGTTTTTCA CTTGCTTTTT ATCCAATGTC CTACTATAGT	600
GCTGCAACAG GAAGTTTGGG GGTATCGGTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTTGATT TTACTTCTAA AATTTTAGAG AATATGTTTT TTTAAGG	707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTTGAA AAACCATACC GATTGACGA CGTATATCC AAACATTTTC CTCAGTCAAA	60
CGTTGGCCAT CAATTACAAAT CTCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAAATCGA	120
ACCGTCGTGT AATTACCACT ACCATTATGC CCTACAATCG AAAGCCATTTC TCCACGTTTC	180
ACGTGAAAGT AATATCCCTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTTAC ATCAATTATT GATTTCATTT CGAACCAANT GTCCCTTTAA ATACATAGGC	300
ACTACCCTTG AAATAGTCAT AGCCAGAGTA GATAGTGAAA AATAAGGCTA CATAAAGTAG	360
AACCTGACCA AGCAAAAGTC AATGTAATAG CAAGAAAATA ATGGCAACA TCTGACTAAA	420
AGTTTTAATT TTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACAGGTTT CAACCAATAA	480
AAGCCTTAAA CTTGCTCAGC CTAAGTACAG ACAGATAACT ACTGCAACAA TCCAGGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAAGT TATCCGCCAT	600
AGGATCTGCA AATTTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAATAGTCG GTAATACTGG CAACAGCAAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTTCTT ATCGTFAAAA TAAAGATAAA AATAGGTATA AA	762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAACTA TGAATACAAA TCTCAAGCCC AAACCTCAGC GTTTTGCTTC	60
TGCGACTGCC TTTGCCGTGC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT	120
CAAGTGCTGC AACCGTCATT CTTTGGACTT GGCGAAATTT GGCTATGTCA ATCTAGTCCC	180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT	240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA	300
AATACCACA ACAATTTTGG ATATCGGTTG TGGTGAAGGA TTCTATTCTC GCAAACTACA	360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT	420
CGCGGCTAAA AGTGAAACCA ACTGGGCAGT CAATTGGTTC GTTGGCGACT TGGCACGACT	480
TC	482

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTAA TAAAGTCAAT ACCGTCTCTT ACTTTTCTT AAAAAAGTT TATTATGTTT	60
TTTAAAGGAG GTAAAAACAT GAAAAATAAT AATAAATCG TTGGAGACG TATTCAAAAT	120
ATCCGTTTAA GCCATGGCGA CTCATATGGAA AAATTGGAG AAAAAATTAA TACTAGCAAA	180
GGTACAGTTA ACAACTGGGA AAAAGGTGCG ANTTTACCA AATAAGAAAA CCTACTAAAA	240
ATTGCATCTA TTGAAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT	300
CTACACTTAA AGATTATGGA TTAGTCTCT GAATGTATAA AAAATTATGA TGAGTATAAC	360
TCTTTACAGC ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAAATAC CATTTCTAAG	420
ATTGATTATC AAATTTTCTA CGAAACGATC AAAAAATTTA TTGATTTAGC TATCGAACAA	480
TGAGAGATT TGCAAGGAAA TTTGTTGAAA AATAACGGGT	520

1364

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

GCATCAAATC CGCCATCAAA GAAGTTCTCT GSATTTACCA AGACCAGTCA AATAGCTTAG	60
AAGTGCTTAA TGACAAGTAC AATGTTCACT ACTGGAATGA CTGGGAAGTT GGAGACACGG	120
GAACCATTTG TGAGCGCTAT GGTGCCGTTC TTAAGAAACA CGACATTATC AATAAGCTTC	180
TCAAACAGTT GGAAACCAAT CCTTGAAC CCGCCAATAT TATTCGCTC TGGGATTACC	240
AAGCTTTCGA AGAAACAGAT GGGCTGCTCC CTGCGCCTT TCAGACCATG TTTGATGTTT	300
GGCGTCTTGA TGGGGAATC TATCTGGATG CGACCTTGAC CCAGCGCTCC AATGATATGC	360
TGGTGCCCA CCACATCAAC GCTATGCAGT ATGTGGCTTT GCAGATGATG ATTGCCAAAC	420
ATTTTGGCTG GAAGGTGGG AAGTCTTCT ACTTCATCAA CAACCTCCAT ATCTATGATA	480
ATCAATTTGA ACAAGCTCAG GAATGCTCC GTCGGGAGCC GTCAAACTGC CAACCACGCT	540
TGTTTAAAA TGTTCTTGAT GGGACTAATT TCTTTGATAT CAAAGCAGAA GATTTTGAGT	600
TGGTGGAATA TGACCTGTT AAGCCACAGT TGAAGTTGA CCTAGCTATT TAAAGAATA	660
GAAGAAAGAA GTTGAGAATA ATCCCACTT CTTTGTTC TTAACGTGAT ACGCGCGCAC	720
GAGCTGCTTT TTTACGGTTT TCTTCGATGA AAGCTGCTT TTGCTCTTCT GGTTCGATTA	780
CTTCTTTTT AAATGCGTAT ACTGCACCTG CAACGGCAGC GACAGTCTCT GCGACACCTG	840
TTACAAGACC TTTAGCGAAT CCTTTAGCCA TGAGTCTTCC TCCTTTATAT TCTCAATCAG	900
CCAGCCTCCT CAAGAGTCA CATTTTCTG ACTGACCTTT TTGTGTATA ATAATAGTAA	960
CGAGAAATG GGAATTTTTC AAGGAAGAAA GATGAGAACA AAA	1003

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CGCGACGTAC TATTCAGAT GCCGAGGAAG TGGACCTCAT CCTCGTTGCC GCAACTGGTC	60
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1365

TCAACGCCTT TGAACGCCCT TTGGTCGGCT CTTCATCTGA ATACATACTC CGCCATGCTA	120
AGGTCGATT GCTGGTTGTG AGAGAACAAAG AAAAAACCTT ATAATCACAA AGAAAAGGAG	180
CCCTAGCTC CTTTTGTTT ACGATTATT TCTCTTTTA TGGCOTTCOT AAGCCTTGAG	240
CTGGCGCTGC AGTTCCTTTT TAATAGCAGG TTCGAGGCA TATTTTCTTT CCCAATTATC	300
TGCTTTTAAAG ATTTTATGGG TCACTGGATC AAAATGAGCC TTCCCATCTG GAAAAATTTT	360
CCCCATATTG GCCTGATGSA CAATATCAAA AATACGTTCT GGTCCACCC CCATCAAGAC	420
AAAACTGCCG TAGGTGAAGT AAAGCGTGTC AATCAAGGCA TCCACTTGCC CTATCAAAATC	480
TTGCTGAGCA GGTGCTCTCT TGGCTACTTT ATCTGCTGCC TTATCAAGGG CCTGATGAG	540
TTGCGATACA GCTTGACCAA AATCTTCTTC AGAAGGACTG GCTGCTCGAA CAAACTCCAC	600
CAATTCTCTT ATTTTAAAA CAGCCCTATG GGTGACCC TCTAAMTCCC AAGCTCGAGG	660
TTCTTCTTGG GTTCGTTTAT CCATCATGTG GTGGAAGTC TTGACCTTAT TGAAATGATA	720
GTCAAGCTG ACAAGACTT TTTCTGAAGA	750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC GGATAACCTC CAAAGAATAT TTTTATATTA TAGCAAAGCT TTAAATTGAA	60
TGTTAGATC TTGTTCAAAA CAATCATCAA AACCACGTGG ATGATGGTAT TCTACTAAGT	120
GTTGATCTTG AGGATAAGTG TACTTACCOC CAACTCCCCA GATAAATGGA TGGAAATCGT	180
ATTGCAAGCG ATCTTTTCGC ATTTTCCAAA GTTCTAGAAT CTCATTAGTA GAAGCCATGA	240
AGTTAGACCA GATATCATAG TGAAGTGGGA TAATGACTTT GGTACGAGA TTTTCTGCCA	300
TACGAAGAAG GTCGATAGAT GTCAKTTTGT CTGGATACC TACCGGATTT TCACCATAGT	360
TATTCAAAGC AACATCAATT TTAAGTCTT TACCATGTTT TGCAAAATAG TTTGAGAAGT	420
GAGAACTGCG ACCATGATAG ATGGTCCAC CTGGTGTTC AAAGATATAG TTAACAGCCT	480
TTTGAGCCAT TTCTTCATCT GTAAACGCCA AGCCAGCagT TCACCGCCGT TCTATCAGC	540
ACCGTTCACT GCGAGAGTTA CCAAGCAAGT ACGGTCAAAT GATTCCTACT CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 673 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA	60
GCTCCTCCAT CAGTTTTTTC TTATAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA	120
ATCACAAATGT CAGCGCCTAC TTCTTTTGCA AGGGCAAGTT TGTCATGTGT GATATCGACT	180
GCGATAACAT GAGCATTGAA TACTTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA	240
CCAGCACCGT AAAGAAACAAC CCATTGGCCT GGTCAACTT TTGCTCTTTT GATAGCTTTA	300
TAGGTTGTTA CTCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA	360
ACTTTGACAG CATAGTCAG AGTTACGATA CATGTGTCAG CCATACCACC GTCTACTGAG	420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCGAA	480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC	540
ACATCTGGAG CAATCTCTTT AACGATACCG ATACCTTCGT GCCCAAGAAC ACGTCTTGGG	600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGTCCGGTGT GGCRAACGCC CACAGTATTTC	660
ACTTCTACAA GTG	673

(2) INFORMATION FOR SEQ ID NO: 349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTACCTTACA AATGCTTTAC AGTATGGGTT GAGGGTGCTC AATGGAAC TAAGTAGGT	60
TGGACAGGAA CTTTGGATA TTCTGATTAC TTACATCTTA CTCGATATCA TACAGCAACT	120
GTTAGACATG GGGGTAGAAC CTCTAAGGAT TATGCAAAAC CTGAGGCATG GCGTAGAGCT	180
TCCCTCACCA AGATTCCG	198

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 891 base pairs
 (B) TYPE: nucleic acid

1367

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCYA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG	60
GACCAATCCA CTACTAATCC TAAGAACAAA AACTCAAGA GAGCAGAAGA GAGAGGTTCA	120
CTGGCACTGA TAACGGCAAC CACCAAGGA GAAACCANGG ACACAGCCTT CATGGAATG	180
AAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA	240
TCAAGAGTAA AGGAAAGCTG ATAAACCGCG GAGAGGACAT TGCTAAACAA ACCTGCCAAA	300
ATCATCCCC ACCCAACCGT AGGAACAAA CCATAAGCT TAGCAAAAGG TTGGGGCAAG	360
ATAACATTAA ACATAACACC CATGGCACTC AGCAAACTG TTATAAGAGC TAGCGCGTC	420
ATGGATACT GAGAGAGGTC TCCCTTTGTC GCCATCAAGC AAACCCCAAC CATGCCAAC	480
AAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTGAT AAACCAAGCG ATTGTAAAAG	540
AGGATAAAGA CAGGCTAAT AAACGTAAA ATAGTTGCTG TCGTAGCATT TGAGTATCT	600
ACACAGAGAT AGAAAAAATA CTGAAGTAA AAAATCCCCA AAATAGCATA GGCTAAAAAG	660
GGCAGGTAAT TTTTCTTGTC TCGCCAAATA TCTAGCACTT GCGATTTTAA TTGTATTGCA	720
GACCAATGA GTACAAGACT CCTGCGAGT GTCAAAAGCA TAGAGGTAAT CCAGCCCGAA	780
GACACCTGAT AATGAGTAAA GAAGTACTCT CTTAAATTC CACAGATTCC CCATATTAA	840
CCGGATAGGA GCGAATAAAT TTTTCCGTTA ACAATCTTTT TCTGATACTG A	891

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCGTTC AATAGAACAT TGCTTTTTTA TTTTAGAGT AAGCTAAGCG CTTGACATC	60
TGCGATGATG GTTACATCAG GGTGATTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC	120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTTGAC TCACCTAAG CAAAAGAAT	180
AATAGACTTG GCATCCAAA TGTITTTAAT CCCATTGAA ATAGCTTGGG TTGGGACGTC	240
TTCAATCTTG GCAAAGAGC GTGCATTGGC TTGATAGTA GACTGGTCAA GTTCTACTAG	300

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ATCGGTTTGA CTGTCAAATG GAGTG 325

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAGAGCACT TTGATGATTT TTGATAGCA TCGAATTTA AAATACAAAT ATGGCAATCG	60
CAGGTTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTCG	180
AGTCAGTAGA TCCGTTTACT GCGGAATAA ATAAGAGGAA GTAAACGTAA GTGCTTTAGC	240
ACTGTCTCGG GAAAGTGGTG CGCGAGGAGG CTATTTTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCGAGA CTACGACACT TCACACTGGT GGT	344

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAAACTT TGCAATCGGC TTGATTCTAC TGCTTTTAGA	120
CCGAGAGAGG CTGTACTTTC TGCTGACTC TATCTCTTC TAGGTGCTAT CGGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTTGAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGTT	300
GTTAAGATTT TTCTTGCAAA CCTCTTGGGT GATGCCCTTG TCTTTGTGG GGGATTCTC	360
AGCTTGCAAT TCCTAGCTGG AATGGCATTT GAAAAAGCTC TTGCTGTGGG GGTCTCTCCC	420
TTTATCATTC CAGACCTTGG CAAACTTCTA GCTATTAGTT TTATTAGCGC TCCCTACTTT	480
CAACGCCTTA AAATCAGGC TTACTTTTACT AACTAAAAA GGATATCGAG TTATCATGAC	540
TCATATTCCT TTCTTTTAT TTGAAAACT TATACTCAAT GAAAAACAA GAGCAAACTA	600
GGAGCTAGC CGCAGGCTG CAAAACACTG TTTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATACGGCAA GGCAAAGCTG AC

692

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1005 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA AACGCATCCA GAAGATTITT TCGATAATGT CGGACCTCTT 60
 GTAGCCAGTA ACTTTTTTCA TACTTACACC GAAGATTITC ACTTGATGAA GGAJATTGGA 120
 GTTAAATCTT TCCGCACTTC CATCCAATGG AGTCGACTCA TCAAGAATTT AGAGACAGGT 180
 GAGCCTGATC CAAAAGGTAT TGCTTTCTAC AATGCCATCA TTGAAGAAGC TAAAAAGAAC 240
 CAGATGGATC TTGTGATGAA TTTACATCAT TTTGATTTC CAGTGGAACT TCTTCAAAAA 300
 TACGGTGGTT GGGAAAGCAA ACATGTAGTG GAGTTATTGC TGAAGTTGC CAAGACTGCT 360
 TTCACATGCT TTGGAGATAA GGTTCATFAC TGGACAACCT TCAATGAGCC AATGGTCATT 420
 CCAGAAGCAG GGTACTTATA TGCTTTCCAT TATCCAAATC TAAAAGGAAA GGGAAAAGAG 480
 GCCGTACAAG TCATCTATAA TCTAAACCTT GCTAGTGCAA AAGTGATTCA ACTATATCGC 540
 TCATTAGAAC TTGATGGAAA GATTGGGATT ATTTTAAACT TGACACCTGC TTATCCAAGA 600
 AGTAATTCTC CAGAAGACTT AGAAGCAAGT CGATTTACAG ATGACTTCTT TAACAAGATC 660
 TTCTTGAATC CAGCTGTAA AGGAACCTTC CCAGAAAGAT TGGTAAAAA GCTAGAGAGA 720
 GATGGCGTGT TATGGAGTCA TACCGAAAAA GAGCTTCAAC TGATGAAATC AAATACGGTT 780
 GATTTTCTTG GAGTAAACTA CTACCATCCA AAACGTGTTT AAGCACAAGC AAATCCTGAG 840
 GAATATCAGA CGCCCTGGAT GCCAGACCAA TACTTCAAAG AGTATGAATG GCTGGAGCGT 900
 CGCATGAATC CATATCGTGG TTGGGAAAIT TTTCGAAAG CCATTATGA TATTGCTATG 960
 ATTGTGAAGG AAGAATATGG TAATATCCCA TGGTTTATCA GTGAA 1005

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 973 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAAA GAGTAAACTA TTAAGTAGTT AATTAAACGG TTTATTACTT	60
TATAGTGAAT CAATATACAT TAAGAAAAGA GGAAGAATG AAAATTAAATA AAAAATATCT	120
AGCAGGTTCAG GTGGCAGTCC TTGCCCTAAG TGTTTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATCAGAGCTCG	240
TCAAAAGGCA GAAAACTTGA CACCAGATGA AGTCAGTTAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGATTA CGGATCAAGG TTAAGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTT CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCAATGAA ATCAAGGGTG GTTATGTCAAT	480
TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATGCGG ATAATATTGG	540
GACAAAAGAA GAGATTAAAC GTCAAGACCA GGAACGCACT CATAATCATA ACTCAAGAGC	600
AGATAAGTCT GTTGCTGCAG CCAGAGGCCA AGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCTTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGGAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAAATCC	840
AGCTCAACCA AGATTGTGAG AGAACCACAA TCTGACTGTC ACTCCAATTT ATCATCAAAA	900
TCAAGGGGGA AACATTTCAA GCCTTTTACG TGAATTGTAT GCTAACCCCTT ATCAGAAGCG	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCCCATCT GCAATATCTG TCGCCTCCAC ATAGCGACA CCAGCCCTGT CTGCTGCCCG	60
TTTGACAGT TCTGCAGATT GACCCAGGAT GACCATCTT TTAGTCCAG TAATGTCTGG	120
CACCAATTCG TCAAACTCAT TGCCACGGTC CAAACCACCT GCARTCAAGA CGACCTTGCT	180
GTGTGCAAA CTGACAAAGC TTTTGAAGTA GCCAAGATAT TAGTTGATT ACTGTCTGTA	240
TAGAATTAA CACsCTTGAT GTCATCCACA AACTGGAGAC GGTGTTTGAC ACCACCGAAG	300
GCTGAAGAGG TTTCTTGAT GCTTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

1371

GTCGCAAGG CATTTCAC ATTGFGGCTA CTTGGAACAC CGATTTCAT CGCTGCCATG 420
 ACTACTTCAC CACGGAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTTCA 480
 AGTGTGAAA ATGOTACAAC AGTGGCTTCT GTCTTGGAAG TCAAGTCTTT TGCCAACTCT 540
 TGATTAAGT TCAAGACAAG GAAATCAGCT GCTGTATCT TGTCTGGAT ATTCCACTTG 600
 GCTGCTACAT ATTCCGAAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTGTGTA 660
 ATAAACGCAA TCTCTGGATG GAATTCCTGA ACACCCATGA GTTGGAAAGA AGAAAGTTC 720
 ATAAACAGG TGTCCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA 780
 TTCCCTGATA AAGACCATG TTGGCCAGCA CGAGTCAAAA CTTCOCGGGn TCCTCTAGAG 840
 TCG

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTAT ATTTTTTTTA TTTATTATTT TTTGGCAAAA AAGACCAATT TGCTTTGGAG 60
 CATTGCTTCT GCATTAAATT GTCTATTTTT GCTCGTGTCT TTACGCTCTT TGTATCATGT 120
 ATTAACTAGC AAGTGCACCT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGOTTATG 180
 ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCTGAATG CTAACCAAGC TAAACACGAA 240
 GTACTTGAAG TACCTGCATC AAACATCAAA AAAGGGATTG CTGAATCCT TAAACCGGAA 300
 GGTTTTGTA AAAACGTTGA AATCATTGAA GATGACAAAC AAGCGTCAT CCGTGATATT 360
 CTTAAATACG GACCAATGAG TGAGAAAGTT ATCACTAATC TGAACGCTGT TCTTAAACCA 420
 GGACTCGTG TCTACAAAA ACGTGAAGAC CTTCCAAAG TTCTTAACGG ACTTGGAAAT 480
 GCCATCCTTT CAACTCTGA AGGTTTGCTT ACTGATAAG AAGCAAGCCA AAAGAATGTT 540
 GGTGGTGAGG TTATCGCTTA CGTTTGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA 600
 GCAAAATTAG GAAGTTGGAG AAGTTTGTTT ACAAACAGGC CAACTTATCT ATTTTGCACA 660
 GTTCTTAGAG CGTGTCAGT TCAGCTCTTG AGCTAAGTAA GTATCTGAAC CCGGTGAAAA 720
 CTGGCCGTGC TGGCATGTTT GGGTAACAGG AGAATAATAA CATGTCACGT ATTGGTAATA 780
 AGTTCAGCTA AGGCCTTCGT AAAAGTT 807

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(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATTT TTGTCCAAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC	60
TTAACCATCT tTGAACAAAA TCCTCAGGCT CAGOTCACTA TTTTCGGTGC CTTGGGTGGC	120
CGTATTGACC ATATGTTGGC CAATGTCITT CTGCTAGCA ATCCTAAGTT GGCACCCTAT	180
ATGCATCAAA TAGAAATTGA GGATGGGCAA AACTTGATTA CTTATTGTCC AGAAGGAATC	240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC	300
CAAGTATGAG TTGACAGAGG AAAATTTTTC CTTTAAAAAA GTGTACGCTT CTAACGAATA	360
TATAGATAGG GAAAGTCCG TAACTTGGCC AGATGTTAT GTGGTGTAC TGCATAGCAA	420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTATTATT AATTGCCAAT CTAGCTGCTC	480
TCTTTCTGAT TTGGCAAAG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGGAGG	540
ATCAGGCAGA TCATTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAGCCA	600
GCCAGTTAGA CCAAAAAGAT TTGGAAGTGG TTGTCAGCA CCGTTTGCAA GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCAGCCAT COTGTGCAAT	60
GACTCTTCCC GATGTAACTT TGTTCATACT CCTTTGATGA ATATGTTCAA GCTGTAGAAG	120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGCGAGTT GACCACTCAG GAAACAGATG	180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCGCATTTA CCTAAACAA GCCTTCCAAG	240
AAAATAGCAA CCTCTAGAG CAAGTGGTAG AACCTTGAC TATTATCACT GGTGGACACA	300
ACCACAAGGA CCAGTTGACC TATGCTTGA AAACACTTTT GCAGAAATGCG CCACATGATA	360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCCGGAGAT GGAAACGCGT TTGCGCAAGG	420

1373

TCAACCAAGT AGGAAACCTTT GTTAAAGAATA ACTTGTCTCAA CGAGTGAAG GGTAAAATTC 480
 CTACGGATAA GGCTCAAAGT GACTATCTCT TTAAGTGCAT TAACACAGGC TTGCATGATA 540
 AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC 600
 CAACAGAAGG CTACAAAAAG ATGGCTGCTC TTATCTTGCC G 641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1958 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTTGAAGG CTCFAAACA ATGGAAGAAT GCTACACAGA TGTGACAGAA 60
 TTTCGCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTTGAAG TGGCTTTAAT 120
 AGCGAAATTA TTGCTTTTAA TCTTTCGACT TCACCCAACT TAGAACAAGT ACAACAATG 180
 TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAATACGA TTCTCCATAG TCACCAAGGC 240
 TGGCAATATC AACACGATTC TTATCATCGG TTCTTAGAGA GTAAGGGAA TCAAGCATCT 300
 ATGTCACGCA AGGCAACAG CCAAGACAAC GGTATGATGG AATCTTTCTT TGGCATTTTA 360
 AAATCCGAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA 420
 GCCATTTATG ACTATATTGA TTAACAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA 480
 CTTAGTCTTG TGCAGTACAG AACTAAATCC TTGGATATAA TTAATTGTCT AACTTTTTGG 540
 GGTCAGTACA AAACCTCTGC TACTATCGGT TTTATTATTG AAAGACCTAT TGGACTTTCT 600
 CTCMAATCGA GTTTTACTC AATTTTCTTA CTGATTGGG ATTGAAATTC CAATTAATTT 660
 CTCTGAGTAG AGTGCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTTT 720
 CAAGAAAAAT TCTGAATGG TTTCGATTC AGGCTACAGA ATAGCACGGT GTTTGTTTGA 780
 GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAAATA ACATCTGTAT TCCCTGCAGA 840
 ATAAACCTCA ACAAGGCTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCAGATG 900
 TGAGTTTCTC GTATTGATAA GCTTCATAAT ATTTCTCCG ATTTTCTAAT TCTATTATAG 960
 CACTTTTGA ATAAAGTGC TTGATTTATA CTCAATGAAA ATCAAGAGC AAACAGGAA 1020
 GCTAGCCGCA GGTATACTT GAGTACGGTA AGGCGAGCT GACGTGGTTT GAATTTTATT 1080
 TTGGAAGAGT ATTAGCCAA CTATATGCTG TTTTTCGAAG ATCAATGOC CCAATTTATG 1140

1374

CTACCACGTT TAAGGTTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTTGTC TTTCTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGAATTG	1260
TAGTAGTAGG TATCAGGATG ACGAGAATAG AAATATTTCGT CAGCTTGTCG GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACTGT CTTCAATTC TCCACATGGT AGGAACCAAG CACCATTGG TCTTTGAACA	1440
AGAACATTT GTTTTGTTC AGGATTAGGG ATAACTGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTTT TCTCCGAAAG TTGGGTTTGC CATTCGATT TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAATCAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTCCA AATCTCAGT AATACCATT ATTGGCTGGTT	1740
AAAGCTAAA GAGAAAACG GAGAGCTAAA CCACCAAGTA AAAGGAATA AACCAAGAAA	1800
GGTGTATGA GATAGACTTA AAAACTATCT TACTGACAT CCAGAGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
LACACTCGAA AAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAAC AAGGATATAG	60
CTTAGAGAAAG CTTTCAAATA AATTTGGGAT AmCAATTC TATCTTAGGT ATATGATTAA	120
ATTGATTGAT GGTACGGAA TAGAGTTCTG CAAAAAAGA AAAAACTGTT ACTATTCTCC	180
TGATTTAAAA CAAGAATGA TTAATAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGAA TACGGTCTCC CAAGTCGTAC GATATCTCTT AACTGGCTAG CACAATACAG	300
GA AAAACGGG TATACTATTG TTGAGAAACC AAGAGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCTTAAA AAAGTAAAGA GAATCCGAT TGAAGGAGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTTGT TANGAATTA TGACTGAGTT TTCGTTAGAT CTCTTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACIT GAAACAGCTA GATAAACAG ATAAGGACCA	540
AGAGCTTAAA GCTGAATTC AATCCATTT TATCGAACAC AAAGGAAT TATGCTTATCG	600

1375

TCGGATTAT TTAGAACTAA GAAATCOTGG TTATCTGGTA AATCATAAA GAGITCAAGG	660
CTTGATGAAA GTACTCAAT TACAAGCTAA AACGGACAG AACGAAAT ATCTCTCTCA	720
TAAAGGAGAC GTTGCCAGA AGGCAGAGAA TCTCATTCAA GCGCAATTTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTTGCC ATTCCAGTAA GTACTTAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGATC GATATCTCCA ATGAGTTGGT TTAGCTGGTA AACTGTAAA AAGATTTCGW	60
CCAATTCAAG GTTGAGGCAT CGCAAACTAT GGACTTTTC CTCGTAGTT CTGGAAGAA	120
AACGGGATAA GGTGGCTGT GAAGCAAGCT GCCCTCCTC CAACAMTTT GGAAGGTAGG	180
CATCAGCTGA CAATCTCTTA CAAGCATAGT CGTTCCTATA ACCTGTAAAC AGTTGAAAGA	240
GGAATCGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCTTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCCG TCTTTTAGTT TCAACTGGGA AAAAAAGTTC TGA AAAAAGA	360
TAAAGACACC ATACTGGGTT AATGACCTC CATCGAAGA TAGTTGTTAA AAGACTTGT	420
TTTGGAGTG ATGATTTGOT AACTGTICA TGTGATTTT CTTCTTTT GTGTTTTTT	480
CTACACTTAT ACCATAAAGG GGAACCTCTT TTTTGCTAG TAAAAACAC CCATTGGGTG	540
AAAAAAGAAA CCAATCCAGA TCTAAGCTAA GCGAAGGATT CTGGATGGTT TTTAGATTG	600
GGGTGAATAA TTGGGTTTT AGCTGCTTGC GGCATTCAG GTTCAGATAC AAAAATTCAC	660
TCATCAACCT TTAGTGAAA TCCAACATA TTAACTATC TATTAGACTA TTACGTGAT	720
AATATAGTCA ATTGAJAAAC GAACAAGACA AAAGAGCTC ATAAAAGATA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGTATAT GAGCCCATGT TTCTCAATA GGATGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATACCCAAA CTCTTCACAC AAGATTCTA	900
ACTTACCCTT TCTATGGAAT CTTCGACTAT CCATAATAA AACCGATGT GTGTTTAATG	960
TTGTTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GCTCTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAACT TCACCATTTG TTAGACTTGC AACCAAGAA ATCTCTGAT	1080

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ATCTTCITCC AGATACITTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTTCTC	1140
GATAAAATA AGTATCGAAT CCTGTTTC	1168

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTGAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGGCT CCGCTTCAGC	60
GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCCTCG GCTTCAGCAT CAACGAGTGC	120
GTGCGCCTCA GCAAGCGCAA GTACCTCAGC GTGAGCTTCC GCCTCAACCA GTGCGTCGGC	180
TTGAGCAGAG ACAAGTGGCT CAGCTTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC	240
GAGTGCGTCT GAGTCAGCAT CAACGAGTAC GTGAGCCTCA GCAAGCAGAT CAGCTTCTGA	300
ATCTGCATCA ACCAGTGGCT CAGCTTCAGC ATGACAAAGC GCCTCAGCTT CAGCAAGTAC	360
CAGTGCCTCA GCCTCAGCGT CGACAAAGTGC GTGCGCCTCA ACCAGTGCAT CTGAATCGGC	420
ATCAACGAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC	480
ATCGGCTTCA GCATCAACCA GTGCGTCGGC TTCAGCGTCA ACCAGTGGCT CAGCTTCAGC	540
AAGTACCAGT GCTTCAGTCT CAGCATCAAC AAGTGCCTTCA GCCTCAGCAT CGACAAAGTGC	600
CTCGGCTTCA GCAAGCAGAT CAGCATCTGA ATCAGGCTCG ACAAGCGCCT CAGCTTCAGC	660
AAGTACCAGT GCGTCAGCCT CAGCGTCGAC AAGTGCCTGA GCCTCAGCAA GTACTAGTGC	720
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCGGGCTCA ACCAGTGCAT CAGAGTCAGC	780
AAGTACCAGT GCGTCAGCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAAGTGC	840
GTGCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCCTCA ACCAGTGGCT CAGCCTCAGC	900
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCG GCTTCAGCAA GTACTAGCGC	960
CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGGCT CTGAATCGGC	1020
ATCAACGAGT GCGTGCCTTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCAT CAACAAAGTGC	1080
ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	1140
GTCAACAAAGT GCATCGGCTT CAGCGTCAAC GAGTGCCTCT GAGTCAGCAT CAACGAGTGC	1200
GTGAGCCTCA GCAAGCAGAT CAGCTTCTGA ATCTGCATCA ACCAGTGGCT CAGCCTCAGC	1260
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCCTCA GCTCAGCGTC GACAAGTGCs	1320

1377

TCGCTTCAG CAAGTACCAG TCGCTCAGCC TCAGCAAGTA CCAGTGCKTC AGCCTCAGCG	1380
TCGACAAAGT CGTCGGCTTC AACCAGTGCA TCTGAATCG CATCAACCAG TCGCTCAGCC	1440
TCAGCAAGTA CTAGCGCTTC AGCCTCAGCA TCAACGAGTG CGTCGGCTTC AGCAAGTACT	1500
AGTGCAATAG CTTCAGCAAG TACTAGCGCC TCAGCTTCAG CGTCGCAAG CGCCTCAGCT	1560
TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAAGT CGTCGGCTTC AGCAAGTACC	1620
TCAGCGTCTG AATCAGCATC AACAAATGCG TCGGCTTCAG CATCAACGAG TGCATCAGCT	1680
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAAG	1740
AGTGCTTCAG TCTCAGCGTC AACCAGTGCC TCTGAATCG CATCAACAG TGCCTCGGCT	1800
TCAGCAAGCA CCAGTGCTTC GCGTTCAGCG TCAACGAGTG CGTCTGAGTC AGCATCAAG	1860
AGTGCCTCAG CTCAGCAAG ACATCAGCTT CTGAATCTGC ATCAACAGT GCGTCACCTC	1920
CGCATCAACA AGCGCTCGG CCTCAGCAAG TCAAGTGCT TCAGCTTCAG CATCAACAG	1980
TGCATCAGCT TCAGCCTCAA CAAGTGCTTC AGCCTCAGCG TCAACGAGTG CCGCGCTTC	2040
AGCAAGTACC AGTGCGTCAG CTTCAGCAAG CACAAGTGCG TCAGCTTCAG CATCAACAG	2100
TGCTTCGGCT TCGGCATCAA CAAGTGCTTC AGCATCAGCA TCAACGAGTG CGTCACTCA	2160
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACCAGTGATC CAGCCTCAGC AAGTATCTCA	2220
CGCTCTGAAT CGGCATCAAC GAGTGATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA	2280
GCCTCAACCA GTGCATCAGT CTCAGCAAGC ACCAGTGCGT CGGCTTCAGC ATCAACAGT	2340
GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGCAT CAACGAGTGC GTCAGCTCA	2400
GCAAGTACTA GTGCATCAGC ATCAGCATCA ACAGTGATC CGGCTTCAGC AAGTACCAGC	2460
GCCTCAGCTT CAGCAAGCAC CAGTGCGTCA GCCTCAGCAA GTACCAGCGC CTCAGCTCA	2520
GCAAGCACCA GTGCTCAGC TTCAGCAAGT ACCAGTGCGT CAGCCTCAGC GTCGACAAAT	2580
CGCTCGGCTT CAGCAAGTAC CTCAGCGTCT GAATCAGCAT CAACGAGTGC ATCAGCTTCA	2640
GCATCAACAA GTGCTTCAGC TTCAGCAAGT ACCAGTGCGT CGGCTTCAGC ATCAACAGT	2700
GCTTCAGTCT CAGCGTCAAC CAGTGCTCTT GAATCAGCAT CAACAGTGC CTCGGCTTCA	2760
GCAAGCACCA GTGCTCGGC TTCAGCAAGT ACTAGTGCAT CGGCTTCAGC ATCGACAAAT	2820
CGCTCTGAAT CGGCATCAAC GAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCAGCTCA	2880
GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCGT CGGCTTCAGC GTCACCAAGT	2940
CGGTCGGCTT CAGGTCGAC AAGTGCTTCG GCTTCAGCAT CAACGAGTGC GTCGGCTTCA	3000
GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCCGC TTCAGCAAGC	3060

1378

ACAAGTGCST CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCGGCTT CAACCAAGTGC GTGGGCTTCA	3180
GCAAGCACAA GTGGCTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCCTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGGCTCAGC CTCAGCATCG ACAAGGCGCT CAGCTTCAGC AAGTACCAAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGGCTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTGGCT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAAGTGC CTCGGCTTCA GCGTCAACCA GTGGCTCAGC TTCAGCAAGT	3540
ACCAGTGCCT CAGTCTCAGC ATCAACAAGT GCTTCAGCCT CAGCATCGAC AAGTGCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTGGCT CAGCCTCAGC GTCGACAAGT GCGTCAGCCT CAGCAAGTAC TAGTGATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTGGCT CAGTCTCGC ATCAACAAGT GCGTCGGCTT CAGCAAGCAC CAGTGGCTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGGCTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGSC ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCGCTCA	3960
GCGTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA GTGGCTCTGA ATCGGCATCA	4020
ACGAGTGGCT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAGTGATC CGGGTTCAGC GTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTGGCTCA	4200
CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACGAG TGCGTCACTT CCGCATCAAC	4260
AAGCGGCTCG GCCTCAGCAA GTACAAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCTT CAGCCTCAGC GTCAGACCAG TGCGTGGCTT TCAGCAAGTA	4380
CCAGTGGCTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGGC	4440
TTCGGCTCA ACAAGTGCTT CAGCATCAGC ATCAACGAGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC	GTCCCTCCGC	CTCAACCAGT	GGCTCCGCTT	CAGCAAGCAC	AAGTGCCTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGCGTCCGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACTT	CCGCTCAAC	CAGTGCCTCG	GCCTCAGCAA	GCACAACTGC	180
GTCACTCTAG	CAAGTATCTC	AGCGTCTGAA	TGGGCATCAA	CGAGTGCCTC	TGAGTCAGCA	240
TCACGAGTA	CCTCAGCCTC	AGCAAGCACA	TCAGCTTCTG	AATCGGCATC	AACCAAGTGG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCTTC	AGCCTCAGCG	360
TCGCAAGTG	CGTCGGCCTC	AACCAAGTGA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	420
TCAGCAAGTA	CTAGTGCACTC	AGCTTCAGCA	TCACGAGTG	CATCGGCTTC	AGCATCAACC	480
AGTGCCTCGG	CTTCAGCGTC	AACCAAGTGC	TCAGCTTCAG	CAAGTACCAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGCAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACCAAGTGC	TGCGCTCAA	CAAGTGCATC	TGAATCGGCA	660
TCACCAAGTG	CGTCAGCCTC	AGCAAGTACT	AGTGCATCAG	CTTCAGCATC	AACCAAGTGA	720
TGCGCTTCGG	CGTCAACCAG	TGCATCAGAG	TCAGCAAGTA	CCAGTGCCTC	AGCTTCGCGA	780
TCACCAAGTG	CCTCGGCTTC	AGCAAGCACA	TCAGCATCTG	AATCAGCGTC	AACCAAGTGC	840
TGCGCTTCAG	CAAGTACCAG	TGCTTCAGCT	TCAGCATCAA	CCAGCGCCTC	GGCTTCAGCA	900
AGCACTCAG	CTTCGAATC	GGCTCAACC	AGCGCCTCGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCTTC	GGCTTCAGCA	1020
AGCACAAGCG	CCTCGGCTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAAGTGC	1080
TCAGCCTCAG	CATCAACAAG	TGCGTCAGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACCAAGTGC	1200
TCAGCCTCAG	CAAGTATCTC	AGCGTCTGAA	TGGGCATCAA	CGAGTGCCTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCATC	AGCGTCAACA	AGTGCCTCGG	CTTCAGCGTC	AACCAAGTGC	1320
TCTGAGTCAG	CATCAACGAG	TACGTCAGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCACCAAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCTCAG	CTTCAGCAAG	TACCAAGTGC	1440
TCAGCCTCAG	CAAGTACCAG	TGCTTCAGCC	TCAGCGTGA	CAAGTGCCTC	GGCTTCACCC	1500
AGTGCATCTG	AATCGGCATC	AACCAAGTGC	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGCATCG	GCTTCGGCGT	CAACCAAGTG	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGCATCTCAG	CATCTGAATC	1680
AGCGTCACCC	AGTGCCTTCGG	CTTCAGCAAG	TACCAAGTGC	TCAGCTTCAG	CATCAACCCG	1740

1380

CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACXAGCG CTTGGGCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAAGGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCCTCAG CTTCAGCATC AACAAAGTGG TCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGGCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAAGTGG TCAGCCTCAG CATCGACAAG	2100
CGCCTCAGCT TCAGCAAGTA CCAATGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAAGTGA TCTGAATCGG CATCAACGAG TCGCTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAAGT CTTGGGCTTC AGCGTCAACC AGTGGCTCAG CTTCAGCAAG	2280
TACCAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCAGTCAG CATCTGAATC AGCGTCGACA AGCGCTCAG CTTCAGCAAG	2400
TACCAAGTGG TCAGCCTCAG CGTCGACAAG TGGCTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCTTC GGCCTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAGTGG TCAGTTCAG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGA TCGGCTTCAG CAAGCACCAG TGGCTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAAGTGC GTCACTCAG CAAGTACCAG CGCCTCAGCC	240
TCAGCAAGCA CCAAGTGCCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	300
AGTGCCTCGG CTTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGTCTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCCTCGG CTTTCAGCAAG TACTAGCGCC TCAGCATCAG CGTCAACAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGGCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAAGTGG TCAGCCTCAG CATCGACAAG CGCCTCAGCT	600

1381

TCAGCAAGTA CCAGTGGGTC AGCCTCAGCA AGTACCAGTG CTTACAGCTC AGCGTCGACA	650
AGTGGGTCGG CCTCAACCAG TGCACTTGAA TCGGCATCAA CCAAGTGGTC AGCCTCAGCA	720
AGTACTACGG CCTCAGCCTC AGCATCAACG AGTGGGTCGG CTTACAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGGCTC AGCTTCAGCA	840
AGTACTAGTG CGTCAGCCTC AGCGTCGACA AGTGGGTCGG CTTACAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TGGGTCGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTACGCTTC AGCAAGTACC AGTGGGTCGG CTTACAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCAG TGCGCTTGAA TCGGCATCAA CAAGTGGCTC GGCCTCAGCA	1080
AGCAACAGTG CTTGGGCTTC AGCGTCAACG AGTGGGTCGG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCAGATC AGCTTCTGAA TCTGCATCAA CCAAGTGGCTC AGCTTCGCGA	1200
TCAACAAGCG CCTCGGCTTC AGCAAGTACA AGTGGCTCAG CTTACAGCATC AACGAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAAGTGGCTC GGCCTCAGCA	1320
AGTACCAATG CGTCAGCTTC AGCAAGCACA AGTGGGTCAG CTTACAGCATC AACGAGTGCT	1380
TCGGCTTCGG CATCAACAAG TGCGTCAACA TCAGCATCAA CGAGTGGGTC AGCCCG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTCTG ACCAGCACCC GTTCTGCGA TAATTTCTT TTTACCCATG	60
CGTWTGGCAA GCCAAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTCGGT	180
AATAAGAGG AGTTTCACGT CCTACGTACT GGCACAAAAG CTGGTTTAAT TCCTCTTGGG	240
AACCTGGGTC TGCGTGACTT TCACGGTAGG CCTCTCCAA CTCCAAAACT GCTGTATCA	300
ATGTTTCTGG GACAAACGT CCGCGAATF TTCCGTAAAA TCCATCTTTA TTTGGTTCC	360
GATATGCCAT GCTTTACCTT CTCTATAAAT CTCTAATCT TTTATGATC TTTTGTCCA	420
TCTGTCTCCA CTCGCTCGA TACATCTACT GCATAGGAG TAAAGTGTTG AATTGCTTTT	480
ACTACATTAT CTTCAITTAAG GCCACCTGCG ATAAAGAGG GCTGTGCTAG TCCAGTCCGA	540

1382

TCCAGTTGAC CCGAATCAAA GGGCTGGCCA TTTCCTGCCA CAGGGGCATC AAGAGTAGA	600
TAATCTGCCT GAGAATTGGG GACATGCCCA TTTCATCTA CCTGCACAGC CTGAATACTG	660
GCACAAGGCA AATTCTCAA TAAATCATCT GCCACCTGAC CGTGAACCTG AACCAAGTCC	720
AAGCCGGGGA TCCTC	735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC TCAGCCTCAG CGTCAACAAG TGCATCGGCT TCAGCATCAA CGAGTGCCTC	60
CGCTTCAGCA AGTACTAGCG CCTCAGCCTC AGCGTCAACA AGTGCATCGG CTTCAGCGCTC	120
AACGAGTGGC TCTGAGTCAG CATCAACGAG TGGCTCAGCC TCAGCAAGCA CATCAGCTTC	180
TGAATCTGCA TCAACCAAGT GCTCAGCCTC AGCTCGACA AGCGCCTCAG CTTCAGCAAG	240
TACCAAGTGG TCAGCCTCAG CGTCGACAAG TGGCTCGGCT TCAGCAAGTA CCAGTGGGTC	300
AGCCTCAGCA AGTACCAAGT GCTCAGCCTC AGCGTCGACA AGTGCCTGGG CCTCAACCAG	360
TGCATCTGAA TGGCATCAA CCAAGTGCCT AGCCTCAGCA AGTACTAGTG CATCAGCTTC	420
AGCATCAACG AGTGCATCGG CTTCAGCATC AACCAAGTGA TCAGAGTCAG CAGTACCAG	480
TGGCTCAGCT TCGCATCAA CAAGTGCCTC GGCTTCAGCA AGTACTAGCG CCTCAGCCTC	540
AGCGTCAACA AGTGCTTCAG CTTCGGGCTC AACCAAGCGC TCGGCCTCAG CAAGTATCTC	600
AGCGTCTGAA TCGGCATCAA CAAGTGCCTC GGCTTCAGCA TCAACGAGTG CATCAGCTTC	660
AGCAAGCACC AGTGGTGGG CCTCAGCAAG CACCAAGCGG TCTGAATCCG CATCAACCAG	720
TGCTTCAGCT TCAGCAAGTA CCTCAGCATC TGAATCAGCA TCAACAAGTG CATCGGCTTC	780
AGCAAGCACA AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAAGGAG	840
TGGTTCGGCT TCAGCAAGTA CTAGCGCCTC AGCATCAGCG TCAACAAGTG CTTCGGCTTC	900
AGCGTCAACG AGTGCCTCTG AGTCAGCATC AACGAGTAG TCAGCCTCAG CAAGCAGATC	960
AGCTTCTGAA TCTGCATCAA CCAAGTGCCT AGCCTCAGCA TCGACAAGCG CCTCAGCTTC	1020
AGCAAGTACC AGTGGGTCAG CCTCAGCAAG TACCAAGTCT TCAGCCTCAG CGTCGACAAG	1080
TGGTTCGGCC TCAACCAAGT CATCTGAATC GGCATCAACC AGTGGGTCAG CCTCAGCAAG	1140
TACTAGCGCC TCAGCCTCAG CATCAACGAG TGGCTCGGCT TCAGCAAGTA CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCTCAG CTTCAGCAAG	1260
CACCAAGTGG TCAGCCTCAG CAAGTACCAG CGCTCAGCG TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA AGTGGCTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCCTTC	1440
AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAAG AGTGGCTCAG TCTCAGCGTC	1500
AACCAAGTGG TCTGAATCAG CATCAACGAG TGCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGGCTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TGCGTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAAGT CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAAGTCAT CAGCTTCAGC CTCACCAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAAGTG GTCACTTCAG CAAGCAACAAG TGCGTCACTT CAGCATCAAC	120
CAGTGCCTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAAGCA GTGCGTCACC	180
TCAGCAAGTA CTAGTGCAATC AGCATCAGCA TCAACCAAGT CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCAATCGCT	300
TCAGCGTCAA CCAAGTGATC AGTCTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAAG	360
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	420
TCAGCAAGTA CTAGTGCAATC GGCTTCAGCA AGCACCAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	540
TCAGCAAGTA CTAGTGCAATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCTTCAG CTTCAGCAAG CACCAAGTGG TCAGCCTCAG CAAGTACCAG CGCTCAGCC	660
TCAGCAAGCA CCAAGTGCTC AGCTTCAGCA AGTACCAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGGCTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAGTG CGTCGGCTTC AGCATCAAG	840

1384

AGTGCTTCAG TCTCAGCGTC AACCACTGCC TCTGAATCAG CATCAACAAG TGCTTCGGCT	900
TCAGCAAGCA CCAGTCCGTC GCCTTCAGCA AGTACTAGTG C	941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCCTCAACCA	60
GTGCATCAGA GTCAGCAAGT ACCAGTGGCT CAGCTTCGCG ATCAACAAGT GCCTCGGCTT	120
CAGCAAGCAC CAGTGGCTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA	180
GTGGCTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGCG ATCAACGAGT GCGTCCGCTT	240
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA	300
GTGCGTCTGA ATCGGCATCA ACGAGTGGCT CGGCTTCAGC AAGTACTAGC GCCTCAGCCT	360
CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA	420
GCGCCCTCAG CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT	480
CAGCATCAAC GAGTGGCTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	540
GTGGCTCAGC CTCAGCATCG ACAAGGCGCT CAGCTTCAGC AAGTACCAGT GCCTCAGCCT	600
CAGCGCTCAGC AAGTGGCTCG GCTTCAGCAA GTACCAAGTGC CTCAGCCTCA GCAAGTACCA	660
GTGGCTCAGC CTCAGCGTCG ACAAGTGGCT CGGCCCTCAAC CAGTGCATCT GAATCGCAT	720
CAACCAAGTGC CTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT	780
CGGCTTCAGC ATCAACCAAGT GCATCAGAGT CAGCAAGTAC CAGTGGCTCA GATTCCGCAT	840
GCAACAAGTG CCTCGGCTTC AGCAAGTAC	869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCACAAGTG CCTCAGCATC AGCATCAACG AGTGGCTCAG CTTACGACAG TACTAGTGCA	60
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1385

TCAGCATCAG CATCAACCAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAAAGGAGT CATCAGCATC AGCATCAACG AGTGCATCGG CTTCAGCGTC AACCAAGTCA	180
TCAGTCTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	300
TGCGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAGTG CGTCAGCCTC AGCAAGTACC AGCGCCTCAG CCTCAGCAAG CACCAGTGCC	540
TCAGCTTCAG CAAGTACCAG TGCCTCAGCC TCAGCGTCA CAAGTGCCTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTGCATCAG CTTCAAGTCA AACCAAGTGT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCCTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGAAAAACA GCTCTGGGCG TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACCTGCCTGC	60
GGAAATGGCT AAGATGGGCG TGTTAGAATC TGATTTGATG AATGTGCTTG CAAGGACACG	120
CTTCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAATCATC CTCTTTATCG ATGAATCCA CACCATCATG GGTCTGGTA GCGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG GCGCGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGCACTT ATGAGAAACA TCACCGTGT CAAATCACAG ATGAAGCGGT	480
TGAJACGCG GTTAAGATGG CTCATCGTGA TTTAAACAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAAG CGGCAGCAAC AGTGCAAAAT AAGGCAAAAG ATGTAAAAGC	600
AGACGATTCA GATTTGAGTC CAGCTGACAA GSCCTGATG GATGGCAAGT GGAAACAGGC	660

1386

AGCCGAGCTA ATCGCAAAAG AAGAGGAAGT ACCGTGCTAC AAAGACTTGG TGACAGAGTC	720
TGATATTTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGACTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAATCCCA AAACGGGTTA TCGGTCAGAA	840
TCAAGCTGTT TCAAGCATTA GCCGTGCCAT TCGCCCAAC CAGTCAGGGA TTCGCACTCA	900
TAAGCGTCCG ATTGGTTCTT TTATGTTCTT AGGCGCTACA GGTGTCGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAAGTC GTCAACATTA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAAGTC TTCGGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAGCGCCT CGGCCTCAGC AAGCACTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCAACAG GCCTCGGCTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAAGTC TTCAGCCTCA GCATCAACAA GTGGGTCAAG CTCAGCAAGT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGGGTCAAG CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAAG GCTTCAGCCT CAGCGTCGAC AAGTGGGTCTG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGGCT CAGCCTCAGC AAGTACTAAT	720
GCA"CGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAAGTC CTCAGCTTCA	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGCCTCCG CTTGAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCAATGGCT TCAGCGTCAA CGAGTGGTTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCT CACCTCAGCA	180
TGGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGGGTGAC CTCAGCGTCG ACAAGTGCCT	240
CGGCTTCAGC AAGTACCAGT GCGTCAsCTC AGCAAGTACC AGTGCCTCAC CTCAGCGTCG	300
ACAAATGCGT CGGCTCAAC CAGTGCATCT GAATCGCAT CAACCAAGTC GTCAOCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAAGT	420
CATCAGAGTC AGCAAGTACC AGTGCCTCAG GTTCGGCATC AACCAAGTGC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCTTC AGCTTCGGCG TCAACCAAGC	540
CCTCGGCTTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACCAAGTGC TCGGCTTCAG	600
CATCAAGAG TGATCAGTC TCAGCAAGCA CCAGTGCCTC GGCTTCAGCA AGCAACGAGC	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CTTGAGCAAG TACTTCAGCA TCTGAATCAG	720
CATCAACAAG TGATCGGCT TCAGCAAGCA CAAGTGCTTC AGGCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAAG AGTGCCTCG CTTGAGCAAG TACTAGGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGGCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAAGTGC TCAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCCTC AGGCTCAGCA AGTACCAGTG	1020
CTTCAGGCTC AGCGTGACA AGTGCCTCG GCTCAACCAG TGCATCTG	1080

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTTCAGGCT CAACCAAGTC CTCTGAATCA GCTTCAACAA	60
GTGCTCGCG TTCAGCAAGC CCCAGTGGT CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGGCTCT GAATCGCATC CAACGAGTGC TTGGGCTTCA GCATCAACGA	180
GTGCGTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAAGT GCGTCCGCTT	240

1388

CAGCGTCAAC CAGTGGCTCG GCTTCAGCGT CGACAAGTGC TTCGGCTTCA GCATCAACGA	300
GTGCGTGGCG CTCAACAAGC GCAAGTACCT CAGCGTCAGC TTCGCGCTCA ACCAGTGGCT	360
CGGCTTCAGC AAGCACAACT GCGTCAGCCT CAGCAAGTAT CTCAGCGTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCACT GCGTCAGCCT CAGCATCAGC AAGCGCTTCA GCTTCAGCAA	540
GTACCAAGTGC TTCAGCCTCA GCGTCAGCAA GTGCGTCGGC CTCAACCACT GCATCTGAAT	600
CGGCATCAAC CAGTGGCTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGCG GCGCCAACT CTATGTGACT ACGGATTATT TCCTAGATTG CATGgGGATA	60
AACCAATTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAGGCCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGCTGACGG TTAACGGCCA	240
AGTGGTGGCT GAACTAGCAA CCACTATCAA GTCAGCGGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCAAGCG GTGTGATTTC	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTGTGCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTAC CCGTGGGGTC GTTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATCCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGGTGT AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGCTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAAT AAAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTC	CATCGTACG	CGGAAATCC	CAGCGCTCA	GCCATCAAT	ATCCTATCAA	60
CGTTCTCAA	AAAAGTGACC	GCTCTCTCAT	CATGTTTCCA	AGTGTAGCC	GCCACTCAA	120
CGATGTCAG	GGGGGCGCAC	ACTskATTGC	CAAAATGGCC	AAGTCCCTA	TCATGCCGGT	180
TACCTACACC	GGTCCCATGA	CTTTGAAGGG	CTTGATTAGC	CGTGAACGTG	TCGATATGAA	240
CTTTGAAAT	CCAAATCGATA	TCTCAGATAT	CAAGAAATG	AATGATGAG	GCATTGAAAC	300
AGTCGCCAAT	CGTATTCAA	CAGAATTCCA	ACGTCTGGAC	GAAGAAACGA	AACAAATGGCA	360
CAATGATAAA	AAACCAATC	CACTCTGGTG	GTTTATCCGC	ATCCCTGCC	TCATCCTTGC	420
TATTTATCCTC	GCTATCCTAA	CCATCATCTT	TAGCTTTATC	GCAAGCTTCA	TCGTGAACCC	480
AGATAAGAAA	AGAGAAGAAC	TTGCATAGAA	GAATGAACC	TTGGCCAAAC	AGCTAAGGTT	540
TTCAATTATA	TAGTAGATTG	GwACTAGAA	AGTACACCTC	TACTTCTAAA	ACATTTTATG	600
AAATCGATT	GACTGTCTTG	ATCGATTCTG	CCTAATCTTA	TTTCAATT		648

(2) INFORMATION FOR SEQ ID NO: 377:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT	TTCCAGCATCG	ACAAGTGCCT	CTGAATCCGC	ATCAACGAGT	GCTTCGGCTT	60
CAGCATCAAC	GAGTGCGTCA	GCTTCAGCAA	GCACATCAGC	TTCTGAATCT	GCATCAACCA	120
GTGCGTCCGC	TTCAAGCTCA	ACCAAGTGCCT	CGGCTTCAGC	GTGACAAAGT	GCTTCGGCTT	180
CAGCATCAAC	GAGTGCGCTG	GCTTCAGCAA	GCACAAATAC	CTCAGCGTCA	GCTTCGGCTT	240
CAACCAAGTG	GTCCGCTTCA	GCAAGCACAA	GTGCTCAGC	CTCAGCAAGT	ATCTCAGCGT	300
CTGAATCCGC	ATCAACGAGT	CGCTCGGCTT	CAGCAAGGCG	AAGTACCTCA	GCCTCAGCTT	360
CGGCTCTAAC	CAGTGCGCTG	GCTTCAGCAA	GCACAAATGC	GTGACCTCA	GCAAGTATCT	420
CAGCGTCTGA	ATCGGATCA	ACGAGTGCCT	CTGAGTCAGC	ATCAACGAGT	ACGTGAGCTT	480
CAGCAAGCAC	ATCAGCTTCT	GAATCGGCAT	CAACCAAGTG	GTGACCTCA	GCATGACAAA	540
GGGCTCTCAGC	TTCAAGCAAGT	ACCAAGTGCCT	CAGCTCAGC	GTGACAAAGT	GCCTGCGGCT	600
CAACCAAGTG	ATCTGAATCG	GCATCAACCA	GTGCTCAGC	CTCAGCAAGT	ACTAGTGCAT	660

CAGCTTCAGC ATCAACGAGT GUATCGGCTT 1390 690

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1003 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTT CAATATGTGC ACGTTGGAAT GTTAGTCGTT 60
 ATATGGGGGG AACAGAATCC TCTCTTGATT GAAGACAAGC TAGTCATTAG GCTGGTTTGT 120
 CTTTGTGTC AACTGTAGTG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT 180
 TTAGTTTAT CAGTACAAAT TTAACGGGTC AAGATTATTA TACTAGTGGT GTTTTGGGG 240
 CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTATCTACT TACAGTTGTT CTGCTCCAAA 300
 GAGCTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAATG 360
 CACAGGATAA CCTGATGCAT TTTTITAGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT 420
 TAGACAATTT TAAACCCCAA TTATTCACCC CAATCTAAA AACCATCCAG AATCCTTGCC 480
 TTAGCTTAGA TCCTGGATGG TTCTTTTCTT CACULAAATGG GTGTTTTTTA CTAGACAAAA 540
 AAGAGTTTCC CCTTATGGT ATAAGTGTAG AAAAAACAC AAAAAAAG GAAACTCACA 600
 TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCITT TTACCAACTA TCTTTCGATG 660
 GAGGTCAATT AACCCAGTAT GGTGGTCTTA TCTTTTTC A GGAACITTTT TCCAGTTGA 720
 AACTAAAGA GGGATTCTT AAGTATTTAG TAAOGAATGA CCAACGCCGC TACTGTGCTT 780
 ATTCCGATT C AGATATCTT GTCCAGTTCC TCTTCAACT GTTAACAGT TATGGAACGG 840
 ACTATGCTTC TAAAGAAATG TCAGCTGATG CCTACTTTCC AAAATTATG GAGGAGGGC 900
 AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTTCCAG AACTGACGAG GAAACAGTCC 960
 ATAGTTTGGC ATGCCTCAAC CTGAATTGG TCGAATTCIT TTT 1003

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTC TGATTGGTTT GCTCTTACT TTGCTGGGAA TTTTGAGGTA GATCTATGAT	60
TGAAATACTA ATTGTTTITAG CTATTATCCT ATCTCTTCCT TFCATTGTAT TGGTAACATAT	120
ACAAACCCGT CAAAATCAAC TATTTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG	180
CTACTGCKAG AGCAACACCT TGGTCAAGGT GCTCACTTTA TTGGTGAGTT TGGCTTTATT	240
TATTCTACTA TTAACCTTTA TGGTGATPAC TTATAAATAA AAGAAAACTT CAGATMTTCA	300
CCTTTTGTGG ATTGGTCTGA AGTTTTCTTT TTTATACTCA ATGAAAAATCA AAGAGCAAAC	360
TAGGAAGCTA GCCGCackGC TCAAAACACC GTTTTGAGGT TGTAGATATA ACTGACGAGC	420
GACTCAAAAC ACCGTTTTGA GGTGTGAGAT ATAACTGACG AGGACTCAA AACACCGTTT	480
TGAGGTTGTG GATAGAAGTG ACGAGcGACT CAAAACACCG TTTTGAGCTT GTGGATAGAA	540
CTGACGAAGT CGcTCAAAAC ACCGTTTTGA GGTGTGGAT AGAACTGACG AATgctCAAA	600
ACACCGTTT GAGGTTGTGG ATAGAAGTGA CGAAGCgaaC ATATATACAG CAAGGCGAGC	660
CTGACGTGGT TTGAAGAGTA TTAAGTCTTA TATTTTGGT AAAAACTAAC TTTTACTTGG	720
ATGAAGGTTT TTTTTTTT	738

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGCTTTATC AAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAAGC ACTTTAGCAC	60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAAACAGC AATAATTCTT TYGGACGGT	120
TAATAGCATC TTGTCACATA GAGTAGATAG ACACATTTCC TTCTTCGTCT ATATCAATCT	180
TAACACCTGT TTCAGCGATA ATCTGTCTGA TGGTTTCTCC ACCCTTACCG ATGACAATCT	240
TAATCTTTGC CACATCAATC TTGATCGTAT CAAATTTTGG AGCAGTTGGA GCCAATCTTG	300
GACGAACTTC TCGAATGGTT GCTTCAATGA CATCAAGGAT TTCAAAAAGC GCTTTCTTGG	360
CTTGACCAAG AGCCTCCGTC AAGATTTCTG CAGTAATCCC TTGAATCTTG ATATCCATTT	420
GAAAGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA TGCCATATCT CCAAAGTGAT	480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA	540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACACC AGCCATAAGG GCAAGAGTTC	600

1392

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACCTCT GCTACTAGAC	660
GGATAGCGTA GGGGAATTC TCCAAGCTTG GCAGG	695

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAATACAT GCTAATATAT TTAGATACAA ACATTCACAC TTGATAATTT	60
TCACTCATCT TTCATCATTC CTATACAAC TATGCAGTAT AATAGAATA GTTTTCTCAT	120
CAGAATGAGA CTATTTTAAT ATTAGATCCC CAATTATTCA CCCCAAATCT AAAAACCATC	180
CAGAATCCTT GCCTTAGCTT AGATCCTGGA TGGTTTCTTT TTTCACCCA TGGGTGTTTT	240
TTACTAGACA AAAAAGAGTT TCCCTTTTAT GGTATAAGTG TAGAAAAAAA CACAAAAAGA	300
AAGGAAACTC ACATGAACAG TTACCAAAAT CATCACTTCC AAAACAAGTC TTTTACCAA	360
CTATCTTTTG ATGAGGTC A TTAACCCAG TATGGTGGTC TTATCTTTTT TCAGGAACCT	420
TTTTCCCACT TGAACATAA AGAGCCGATT TCTAAGTATT TAGTAACGAA TGACCAACGC	480
CGCTACTGTC GTTATTGGGA TTCAGATATC CTGTCCAGT TCCTCTTTCA ACTGTTAACA	540
GGTTATGGAA CGGACTATGC TTCTAAAGAA TTCTCAGCTG ATGCCCTACTT TCCAAAATTG	600
TTGGAAGGAG GGCAGCTTGC TTCACAGCCA ACGTTATCCC GwTTCTTTTC CAGAACTGAC	660
GAGGAACAG TCCATAGTTT GCGATGCCTC A	691

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGCTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC	60
CAAGTTATGC CTAAGGGGCC TTAGGANTAG GAGCTTTCAC AAGCTTATCC AGATGATTAT	120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAATCAA GTACCTTAAA GATTCGACT	180
AATATTGGCT TTGCATTTAT TCCTCCATAC ACACGAGAGA TGAACCCCAT TGAACAGTG	240

1393

TOGAAAGAGA TTCTGTAACG TGGATTAAAG AATAAAGCCT TTCGAACITTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GTGATATAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTGTGAA ACAGATGAGT ATAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TCAAAATAGA ACAGGATAGT CAAATCGATT TCTAACAAATG	480
TTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTTGGGG AGTGATAGAA	540
AAGCCCTTCA TCAGCCAATC TACTTGTTCA GTGCGAGAG CTTGACATC CTTTCTGTGA	600
CTGGACCAAG TCAGTTTTCC GTTCTCAAAG CGTTTATATA ATATCCAAAA TCTTGACCA	660
TCCAGTAAA GAACTTTAAA GCGTCTTTA CGTCCACCAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAAA GTGGGTTTG	750

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAATTCTT CGTGTCCGC ATATCTTCTT TGTACACGG CAGTCACTTG GTCTTCACT	60
ACTCGAGTGC CAGTTCACG GGCCAATTC TCTTCTACTT GAACTGCCTT TTGGAGTCA	120
CTGTGTAGG CTGCAATGAT TTCAGCTTGC AATTTCAGCAT CCACGTGAAG CAATTCCTACT	180
TCTGCTTTT CTTCACGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCCTTG	240
ACAGCTTCGT GCCCTTAAAG GAGCGCTTCC AACATGATTT CTCTGACAA TCTTTGGCA	300
CCAGACTCTA CCAATGTGAT AGCGTGCTTG GTTCCAGCTA CTGTCAATTC AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGAAT TGGGTTGATG ATGATTTGGC CATCTACATA TCCCACCTGT	420
ACCCAGCAA TTGGTCCGTC AANTGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AACATAGCAG CCATTTGGTG AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGAAAC ATAGAGCGAA TCGGACGGTC AATCAAAAGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAC	660
TTCCAGCCCG CATACATTTT TTCTTCGTAG TTGACTTGGA GTGGGAAGAA ATCCTCATGT	720
GCCATTTTCT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATT ACCGTGGACT AAAGTTGAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT	60
TAGGAACATAT ATATGAGTTC TCTAGTCTGG AGATTTTTC AATAGACTTCG TTATTGGGGC	120
GTTACTTTTCG AAACCTTGAA AACTTCAAAA AACGGATTTT TATCGCTTTC AAATTCCTTT	180
GGGGTCAAAC TCAGTAACTT ATTCGCCCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC	240
AAGGTCCCAA ATAGCCAAGA ATCGTCAOCC ATATTATCTG AATCATCTCC TTCTGTCTCT	300
CCTTTAGTTC GCCTGAGGAC AGCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAGAGGCT	360
TGGTCAGGTA GTACATGACC CCTAATTCCA AGGCCAAAC CTATCAAAT TCATCACTTT	420
TCGCAGAAAC CATCATAAAT GGAGTTTGA CGCCTTGGC TCTCAGCCGC TTACAAACTT	480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTTCGTGTT	540
CTGCCAAAGC TAAGSCCTTC CGTCCATTG TCACCAATTG AGTAGAAAG CCTTCCTTAC	600
TTAAATGGTA GTCAGCAAT TTCAGAAATG GTTCTTCATC ATCCACTAAT AAGACTT	657

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAG ATCAACGAGT GCATCGGCTT CAGCTCAACC AGTGCAATCAG TCTCAGCAAG	60
CACCACTGCG TCGGCTTCAG CATCAACGAG TGCCCTCAGCC TCAGCAAGTA TCTCAGCGTC	120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGCG TTCAGCAAGC	180
ACCAATCGGT CGGCTTCAGC ATCAACCAAT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT	240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCAATCAGCA TCAGCATCAA	300
CGAGTGCATC GGCTTCAGCA AGTACCAGCG CCTCAGCTTC AGCAAGCACC AGTGGGTAC	360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC	420
CAGTGGGTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACTCTC AGCGTCTGAA	480

1395

TCAGCATCAA CGAGTGGCTC AGCTTCAGCA TCAACCAAGTG CCTCAGCCTC AGCAAGTATC 540
 AGTGGCTCAG CTTTCAGCATC AACGAGTGGC TCAGCTGCAG CAAGTA 586

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTTCAGCATC AACAAAGTGCT TCAGCTTCAG 60
 CAAGTACCAG TGGTCGGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAAGTG 120
 CCTCTGAATC CGCATCAACA AGTGCTCGG CTTTCAGCAAG CACCAAGTCT TCGGCTTCAG 180
 CGTCAACGAG TGGCTCTGAG TCAGCATCAA CGAGTGGCTC ACCTCAGCAA GCACATCAGC 240
 TTCTGAATCT GCATCAACCA GTGGCTCAGC TTCGGCATCA ACAAGCGCCT CGGCTTCAGC 300
 AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CACAAGTGC 360
 TTCAGCCTCA CGGTCAACCA GTGGCTCGG CTTTCAGCAAGT ACCAGTGGCT CAGTTCAGCA 420
 AGCACAAGTG CGTCAATTTA GCATCAACCA G 451

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCCTCAGCAAG CACCAATGCG TCGGCTTCAT CAAGCAACG CGGCTTTGAA TCCGCATCAA 60
 CCAGTGCTTC AGCTTCAGCC AAGTTACTC AGCATCTGAA TCAGCATCAA CAAGTGCATC 120
 GGCTTCAGCA AGCACAAGTG CTTTCAGCTCA CCAAGTATCT CAGGCTCTGA ATCGGCATCA 180
 ACGAGTGGCT CGGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGGCTCAAC AAGTGCTTCG 240
 GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTAGCTCAGC CTCAGCAAGC 300
 ACATCAGCTT CTGAATCTGC ATCAACCAAGT GGGTCAGCCT CAGCATCGAC AAGCGCCTCA 360
 CGCTCAGCAA GTACCAAGTGC GTCAGCCTCA CCAAGTACCA GTGCTTCAGC CTCAGCCTCG 420

ACAAG 1396 425

(2) INFORMATION FOR SEQ ID NO: 388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTT ATCATGTAGT 60
 AGACAAATCT TTCATACTCC AACACTTGCC CATTTTATGC GAATCTCATC TATTTTCTCT 120
 TTTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCAITTA CAGTCACGCG CCCAGCCTTG 180
 AGCAAGTTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT 240
 CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCTTTTCG 300
 TTTTCATATC TTCAAAAATC TCTTCAAACC GGGTCAAGCT CGCCTTGCGG TATATATGTT 360
 ACTGACTTCG TCAGTCTTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTGCTCAGT 420
 TCTATCTGCA ACCTCAAAGC AGTGCTTTGA GCATCCTGCG GCTAGTTTCC AAGTATGCTC 480
 TTTGATTTCW ATTGAGTATC AGATTTAGGA AATTAACCTC CTCGKCTCCA AAAAAKAGCT 540
 AAAACAATCA AGGCTCTTAA AATCGCTGGG AT 572

(2) INFORMATION FOR SEQ ID NO: 389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT 60
 CTGAATCAGC ATCAAGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT 120
 CAACAAGTGC TTCGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT 180
 CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCGTCA GCCTCAGCAT 240
 CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT 300
 CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAAGTC ATCTGAATCG GCATCAACCA 360
 GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT 420

1397

CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA 480
GCGCCTCAGC TTCAGCAAGC ACCGG 505

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA COTCATTAGG GOCATAGGCT GCTAAAATAA CTCAGCTGT GGTAAATGAC 60
AATACTGTAC TTTTTCAT TTTAATTCCT TACATATTTA TATAACTTCC AATAGATAAT 120
AACTTTTAACT TTCTAGACC TTTGTTTAA AAGTTTTAC TAAGTATTAT CTAGGAATA 180
GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAA 240
ATTTAAGTCA AAAAAATTA CATTAGTTAA TTTATTTTT AGCACACATT AAAAAATAG 300
ATTAGTACTC AATGAAATC AAGAGCAA CTAGGAAGCT AGCCGAGAT TGCTCAAAAC 360
AGTGTTTCA GOTTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT 420
GGATAGAAGT GACGAAGTCG GTACCGA 447

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCAGTTGTC GTTGAATCT ACAACAAAT GTTGTAAAT TTTATTGAAT AAGTAGGCC 60
TTGATATTA GCACTTTGGG ACGTCTCC TTAGTGCTTT TTTGATTTCT CTAGTATCC 120
AGCTATATC GTTGAGACAT AACTAGACC ATATAGTCCA AACTGATATA GTAAATGAA 180
CCAAAATAG TACAATATG GTTATATCC TTTATGGCA TATTCAATAG ATTTTCGTAA 240
AAAAGTTCTC TCTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCA 300
AATCTCACGT AATACATT ATGGCTGTT AAGCTAAAA GAGAAACAG GAGAGCTAAA 360
CCACCAGTA TAGTGTATTG AATCTATAAC AGTACACTT GCTGCTAAA ATATTTCTAT 420

1398
AAATTAAATT GACTTCCCTG ATAGAGATGT TCACATCTTA TTTCAAACTA CTATATAAGT 480
TCTATAATCT CTTTATAAGA TTGCCCCATC AGACAAAATA GAACGATTTG AAGGCGTTTA 540
TGAATATTAG CTGTACGAGA GTCTTTTAAA AG 572

MISSING UPON TIME OF PUBLICATION

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegians Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

- 25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.
- 30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.
- 35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:
- 45 a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;
- b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
- c) retrieval means for obtaining said homologous sequence(s) of step (b).
- 50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 55

60 7. A method for identifying an expression modulating fragment of
Streptococcus pneumoniae genome comprising the step of comparing a database
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a
representative fragment thereof, or a nucleotide sequence at least 95% identical to
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
65 nucleic acid molecule comprised of a complementary nucleotide sequence to said
target sequence, wherein said target sequence comprises sequences known to
regulate gene expression.

8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*
pneumoniae genome, wherein said fragment consists of the nucleotide sequence of
70 any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a
degenerate variant thereof.

9. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a
75 degenerate variant thereof.

10. An isolated fragment of the *Streptococcus pneumoniae* genome,
wherein said fragment modulates the expression of an operably linked open reading
frame, wherein said fragment consists of the nucleotide sequence from about 10 to
80 200 bases in length which is 5' to any one of the open reading frames depicted in
Tables 2 and 3 or a degenerate variant thereof.

11. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome of claim 8.
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12. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 8.

13. An organism which has been altered to contain any one of the
90 fragments of the *Streptococcus pneumoniae* genome of claim 10.

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;

b) identifying members of said library which contain sequences that hybridize to said target sequence; and

c) isolating the nucleic acid molecules from said members identified in step (b).

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

a) isolating mRNA, DNA, or cDNA produced from an organism;

b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;

c) isolating said amplified sequences produced in step (b).

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of claim 17.

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20. A method for producing a polypeptide in a host cell comprising the steps of:

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a) incubating a host containing a heterologous nucleic acid molecule whose nucleotide sequence consists of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and

b) isolating said protein.

Figure 1

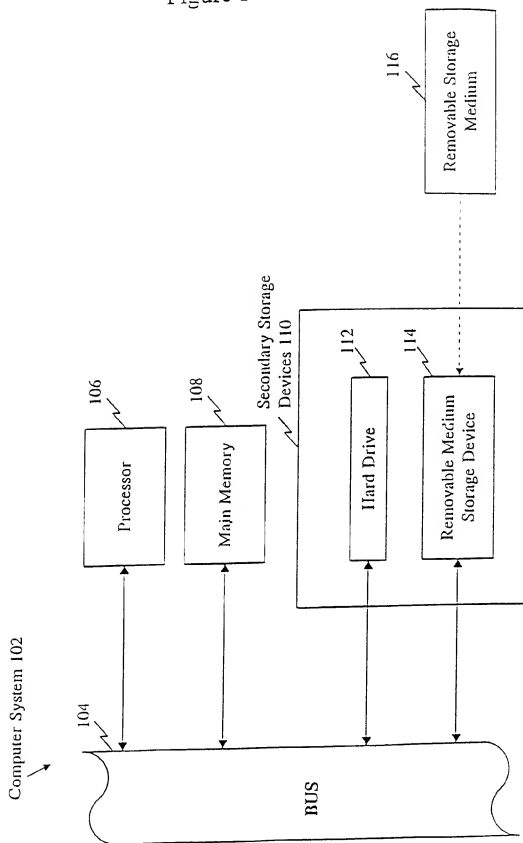


Figure 2

